

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2003, 10:28:47 ; Search time 29 Seconds  
(Without alignments)  
3242.473 Million cell updates/sec

Title: US-09-817-487a-2

Perfect score: 4569

Sequence: 1 MRELVINPLVHILTLVAFSG.....TSIHRLERKCEKRAEQTAVS 869

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published\_Applications\_AA.\*  
1: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB pep.\*  
2: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB pep.\*  
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8: /cgn2\_6/ptodata/2/pubppa/US08\_PUBCOMB pep.\*  
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10: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB pep.\*  
11: /cgn2\_6/ptodata/2/pubppa/US10\_NEW\_PUB pep.\*  
12: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB pep.\*  
13: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB pep.\*  
14: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4569	100.0	869	US-09-817-487a-2	Sequence 2, App1
2	4558	99.8	869	US-10-016-283-33	Sequence 33, App1
3	4292.5	93.9	868	US-10-016-283-1	Sequence 1, App1
4	899	19.7	937	US-09-974-298-129	Sequence 129, App
5	861	18.8	822	US-09-966-147-2	Sequence 2, App1
6	861	18.8	847	US-09-924-859A-5	Sequence 5, App1
7	810	17.7	790	US-09-966-147-9	Sequence 9, App1
8	810	17.7	814	US-09-924-859A-3	Sequence 3, App1
9	807.5	17.7	850	US-09-924-859A-7	Sequence 7, App1
10	792.5	17.3	839	US-09-966-147-6	Sequence 6, App1
11	774	16.9	1070	US-09-961-403-3	Sequence 3, App1
12	741	16.2	641	US-10-242-943-4	Sequence 4, App1
13	695.5	15.2	802	US-10-011-548-33	Sequence 33, App1
14	693.5	15.2	802	US-09-758-386-3	Sequence 3, App1
15	679	14.9	822	US-09-757-415A-2	Sequence 2, App1
16	677	14.8	850	US-09-985-675-2	Sequence 2, App1
17	677	14.8	874	US-09-985-675-1	Sequence 1, App1
18	677	14.8	880	US-09-223-490-10	Sequence 10, App1
19	671.5	14.7	764	US-09-925-302-714	Sequence 714, App

20	671	14.7	874	US-09-158-722-6	Sequence 6, App1
21	662	14.5	850	US-09-985-675-4	Sequence 4, App1
22	662	14.5	876	US-09-985-675-3	Sequence 3, App1
23	662	14.5	890	US-09-223-490-2	Sequence 2, App1
24	662	14.5	911	US-09-924-859A-1	Sequence 1, App1
25	656	14.4	257	US-09-823-187-46	Sequence 46, App1
26	653.5	14.3	1338	US-10-059-585-44	Sequence 44, App1
27	651.5	14.3	374	US-09-205-658-108	Sequence 108, App
28	651.5	14.3	374	US-09-844-353A-108	Sequence 108, App
29	647.5	14.2	1363	US-09-375-248-19	Sequence 19, App1
30	644.5	14.1	1367	US-09-870-759-120	Sequence 120, App
31	644	14.1	297	US-09-939-833-8	Sequence 8, App1
32	644	14.1	297	US-09-939-754-8	Sequence 8, App1
33	644	14.1	297	US-09-939-832-8	Sequence 8, App1
34	642.5	14.1	854	US-09-158-722-20	Sequence 20, App1
35	641.5	14.0	370	US-09-205-658-107	Sequence 107, App
36	641.5	14.0	370	US-09-844-353A-107	Sequence 107, App
37	641.5	14.0	891	US-09-862-027-25	Sequence 25, App1
38	633.5	13.9	1298	US-09-982-610-33	Sequence 33, App1
39	633.5	13.9	1363	US-09-375-248-2	Sequence 2, App1
40	630	13.8	1368	US-10-105-901-34	Sequence 34, App1
41	629.5	13.8	885	US-09-919-497-52	Sequence 52, App1
42	628.5	13.8	888	US-10-281-878-5	Sequence 5, App1
43	626	13.7	894	US-09-223-490-34	Sequence 34, App1
44	624.5	13.7	999	US-10-174-590-434	Sequence 434, App
45	624.5	13.7	999	US-10-176-758-434	Sequence 434, App

## ALIGNMENTS

RESULT 1  
US-09-817-487a-2  
; Sequence 2, Application US/09817487A  
; Patent No. US20020150876A1  
; GENERAL INFORMATION:  
; APPLICANT: No. US20020150876A1artis AG  
; TITLE OF INVENTION: Selectable Marker Genes  
; FILE REFERENCE: 4-31193A  
; CURRENT APPLICATION NUMBER: US/09/817,487A  
; CURRENT FILING DATE: 2002-02-14  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 869  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-817-487a-2

Query Match 100.0%; Score 4569; DB:10; Length 869;  
Best Local Similarity 100.0%; Pred. No. 1.8e+262;  
Matches 869; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRELVINPLVHILTLVAFSGTEKLPKAPVTTTLETVDAIVEVATFMCAVESYPOPEIS 60  
DB 1 MRELVINPLVHILTLVAFSGTEKLPKAPVTTTLETVDAIVEVATFMCAVESYPOPEIS 60  
QY 61 WTRNKILIKLFDRTYSIRENGQLTLISVSDSDGYCCATNGGAVGSCALQVKKM 120  
DB 61 WTRNKILIKLFDRTYSIRENGQLTLISVSDSDGYCCATNGGAVGSCALQVKKM 120  
QY 121 PKITRPPINVKITIEGLKAVLPCTTMGNPKRSVWIKGDSPLRENSRIAVLESGSLRIHNV 180  
DB 121 PKITRPPINVKITIEGLKAVLPCTTMGNPKRSVWIKGDSPLRENSRIAVLESGSLRIHNV 180  
QY 181 QKEDAQCYRCVAAANSIGTAYSKVKLEFEYFAILAPESHNTFSSFTLHCTANGIPV 240  
DB 181 QKEDAQCYRCVAAANSIGTAYSKVKLEFEYFAILAPESHNTFSSFTLHCTANGIPV 240  
QY 241 PTTTWIENGNAVSSGSIQESVSKVDISRLQLEITPKGYLCTATNKHGKSTAKAAT 300  
DB 241 PTTTWIENGNAVSSGSIQESVSKVDISRLQLEITPKGYLCTATNKHGKSTAKAAT 300

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QY 301 ISTAEMSKPOKDNKGCAOYRGEVCNANVLAKDALVFINTSYADPEAEQELLVHTANNEK 360
DB 301 ISTAEMSKPOKDNKGCAOYRGEVCNANVLAKDALVFINTSYADPEAEQELLVHTANNEK 360
QY 361 VVSFVCPAPAEALICNHIPOECSPGVVPTPIICREYCLAVKELFCAKEMLVMEKTHRG 420
DB 361 VVSFVCPAPAEALICNHIPOECSPGVVPTPIICREYCLAVKELFCAKEMLVMEKTHRG 420
QY 421 LYSEMHLLSVPCSKLPSMHMDPTACARLPHLDYNNENKTTPPMTSKSPVDIPLPS 480
DB 421 LYSEMHLLSVPCSKLPSMHMDPTACARLPHLDYNNENKTTPPMTSKSPVDIPLPS 480
QY 481 SSSSFVSPTSMTVITISMSFAIFVLLTITLYCCRRKQKNNKRESAAVTLTTL 540
DB 481 SSSSFVSPTSMTVITISMSFAIFVLLTITLYCCRRKQKNNKRESAAVTLTTL 540
QY 541 SELLDRLHPNPMYORPMLLNPKLSLEYPRNNIEVRDIGEGAFGRVFOARAGILPY 600
DB 541 SELLDRLHPNPMYORPMLLNPKLSLEYPRNNIEVRDIGEGAFGRVFOARAGILPY 600
QY 601 EPTFMVAVKMLKEASADMDQADPQREALMAEPDNPVITVLLGCAYGKPMCLIFEMAY 660
DB 601 EPTFMVAVKMLKEASADMDQADPQREALMAEPDNPVITVLLGCAYGKPMCLIFEMAY 660
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DB 661 GDLNEFLRSMSPHTVCSLSHSDLSMRAQVSSPGPPPLSCAEQOLCIANOVAAGMAYLSERK 720
QY 721 FVHRDLATRNCLNGENNVVKIADFGLSRNTYSADYYANENDAIPIKMPPESTFYRYRT 780
DB 721 FVHRDLATRNCLNGENNVVKIADFGLSRNTYSADYYANENDAIPIKMPPESTFYRYRT 780
QY 781 TESDVMAVGVLMETISYGLOPYYGMAHEEYIYVRGNILSCPCNPVELYNLMRLCWS 840
DB 781 TESDVMAVGVLMETISYGLOPYYGMAHEEYIYVRGNILSCPCNPVELYNLMRLCWS 840
QY 841 KLPADRPSTSIHRIERMCEERAGTVSV 869
DB 841 KLPADRPSTSIHRIERMCEERAGTVSV 869

RESULT 2
US-10-016-283-33
; Sequence 33, Application US/10016283
; Patent No. US20020164702A1
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al., David M.
; TITLE OF INVENTION: NOVEL TYROSTINE KINASE RECEPTORS AND LIGANDS
; FILE REFERENCE: REG195-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/016,283
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US/09/077,955A
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US96/20696
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In Ver. 2.0
; LENGTH: 869
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-283-33

Query March 99.8% Score 4558; DB 9: Length 869;
Best Local Similarity 99.8% Pred. No. 8e-262;
Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRELVINIPLVHILTLVAFSGTEKLPKAPVITTPLETVDALVEEVAIFMCAYESTPOPEIS 60
DB 1 MRELVINIPLVHILTLVAFSGTEKLPKAPVITTPLETVDALVEEVAIFMCAYESTPOPEIS 60
QY 61 WTRKKILKLFDTKYSIRENGQLTITLVEDSDGIYCTTANNVGAVESCGALOYKMK 120
DB 61 WTRKKILKLFDTKYSIRENGQLTITLVEDSDGIYCTTANNVGAVESCGALOYKMK 120

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DB 61 WTRKKILKLFDTKYSIRENGQLTITLVEDSDGIYCTTANNVGAVESCGALOYKMK 120
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DB 121 PKTTRPINNKIIIEGLKAVIPCTTMGNPKRSYSWIKGDSLRNSRTAVLESSLRHNV 180
QY 181 OKEDAGYRCVANKSLGTATSKVYKLEFEFARILRAPESHNTFGSFVTLHCTATGIPV 240
DB 181 OKEDAGYRCVANKSLGTATSKVYKLEFEFARILRAPESHNTFGSFVTLHCTATGIPV 240
QY 241 PTTIWIENGNAVSSGSIQESYKDRVIDSRLOLPTTKGGLYTCTATNKGKSTARAAT 300
DB 241 PTTIWIENGNAVSSGSIQESYKDRVIDSRLOLPTTKGGLYTCTATNKGKSTARAAT 300
QY 301 ISTAEMSKPOKDNKGCAOYRGEVCNANVLAKDALVFINTSYADPEAEQELLVHTANNEK 360
DB 301 ISTAEMSKPOKDNKGCAOYRGEVCNANVLAKDALVFINTSYADPEAEQELLVHTANNEK 360
QY 361 VVSFVCPAPAEALICNHIPOECSPGVVPTPIICREYCLAVKELFCAKEMLVMEKTHRG 420
DB 361 VVSFVCPAPAEALICNHIPOECSPGVVPTPIICREYCLAVKELFCAKEMLVMEKTHRG 420
QY 421 LYSEMHLLSVPCSKLPSMHMDPTACARLPHLDYNNENKTTPPMTSKSPVDIPLPS 480
DB 421 LYSEMHLLSVPCSKLPSMHMDPTACARLPHLDYNNENKTTPPMTSKSPVDIPLPS 480
QY 481 SSSSFVSPTSMTVITISMSFAIFVLLTITLYCCRRKQKNNKRESAAVTLTTL 540
DB 481 SSSSFVSPTSMTVITISMSFAIFVLLTITLYCCRRKQKNNKRESAAVTLTTL 540
QY 541 SELLDRLHPNPMYORPMLLNPKLSLEYPRNNIEVRDIGEGAFGRVFOARAGILPY 600
DB 541 SELLDRLHPNPMYORPMLLNPKLSLEYPRNNIEVRDIGEGAFGRVFOARAGILPY 600
QY 601 EPTFMVAVKMLKEASADMDQADPQREALMAEPDNPVITVLLGCAYGKPMCLIFEMAY 660
DB 601 EPTFMVAVKMLKEASADMDQADPQREALMAEPDNPVITVLLGCAYGKPMCLIFEMAY 660
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DB 721 FVHRDLATRNCLNGENNVVKIADFGLSRNTYSADYYANENDAIPIKMPPESTFYRYRT 780
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DB 841 KLPADRPSTSIHRIERMCEERAGTVSV 869

RESULT 3
US-10-016-283-1
; Sequence 1, Application US/10016283
; Patent No. US20020164702A1
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al., David M.
; TITLE OF INVENTION: NOVEL TYROSTINE KINASE RECEPTORS AND LIGANDS
; FILE REFERENCE: REG195-B-PCT-US
; CURRENT APPLICATION NUMBER: US/10/016,283
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US/09/077,955A
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US96/20696
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In Ver. 2.0
; LENGTH: 868

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TYPE: PRT  
ORGANISM: Rattus sp.  
us-10-016-283-1

Query Match 93.9% Score 4292.5; DB 9; Length 868;  
Best Local Similarity 93.2%; Pred. No. 4e-246;  
Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

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DB 1 MRELVINPLVHILTLVAFSGTEKLPKAPVITPTETDALVEEATMCAYESPOEIS 60  
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DB 61 WTRNKILIKLFEDRYSIRENQQLTLISVEDSDGIYCCTANNVGAVESGALQYKMK 120  
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DB 121 PKTRPPINKKIEGKAVLPCTTMGNPKPSVSIKSDSPREMSRIAVLESGLRIHNV 180  
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DB 181 OKEDAGQRCVAKNSLGTAVSKYKLEFEVFARILRAPESHNTFEGSVTLHCTATGIPV 240  
QY 241 PTTWINGNNAVSSGSIQESVKDRVIDSRQLPFTKGLYTCIATNKGKFTAKAAT 300  
DB 241 PTTWINGNNAVSSGSIQESVKDRVIDSRQLPFTKGLYTCIATNKGKFTAKAAT 300  
QY 301 ISTAEMSKPOKDNKGCAOYRGECVCAVLAKDAVLENTSYADPEEAOELLVHTAMLEK 360  
DB 301 ISTAEMSKPOKDNKGCAOYRGECVCAVLAKDAVLENTSYADPEEAOELLVHTAMLEK 360  
QY 361 VSTAEWSKQESGEGCAOYRGECVCAVLAKDSLVFNTSYPDPEEAOELLVHTAMLEK 360  
DB 361 VSTAEWSKQESGEGCAOYRGECVCAVLAKDSLVFNTSYPDPEEAOELLVHTAMLEK 360  
QY 420 VSPVPCRAAEALCNHIFQECSPGVPTPIPICREYCLAVKELCAKEMLVMEKTHRG 420  
DB 420 VSPVPCRAAEALCNHIFQECSPGVPTPIPICREYCLAVKELCAKEMLVMEKTHRG 420  
QY 480 AYSPLCRPAEALCNHIFQECSPGVPTPIPICREYCLAVKELCAKEMLVMEKTHRG 480  
DB 480 AYSPLCRPAEALCNHIFQECSPGVPTPIPICREYCLAVKELCAKEMLVMEKTHRG 480  
QY 540 SSSSFSVSPYTMVTIISMSFAIFVLTITLTYCCRRKQKNNKRESAAVTLTLP 540  
DB 540 SSSSFSVSPYTMVTIISMSFAIFVLTITLTYCCRRKQKNNKRESAAVTLTLP 540  
QY 541 SELLDRLHPNMYQMPPLLNPKLLSLEYPRNNIEYRDIGGAFGRVQARAPGLLPY 600  
DB 541 SELLDRLHPNMYQMPPLLNPKLLSLEYPRNNIEYRDIGGAFGRVQARAPGLLPY 600  
QY 600 EPTTVAVVKMLKEEASADQADQOREALMAEFDPNPIYKLVCAVKGKPMCLFEYMA 660  
DB 600 EPTTVAVVKMLKEEASADQADQOREALMAEFDPNPIYKLVCAVKGKPMCLFEYMA 660  
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DB 661 GDLNEFLRSMPTVCSLSHSDLSMRQVSSPPPLSCAEOLCIAROVAAGMAYLSERK 720  
QY 720 FVHRDLATRNCLVGENNVYKIAFGLSRNTYSADYKANEANDAIPRMPPEISIFNRYT 780  
DB 720 FVHRDLATRNCLVGENNVYKIAFGLSRNTYSADYKANEANDAIPRMPPEISIFNRYT 780  
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DB 781 TESDVNAVGVLMETISYGLQYRYGMAHEVITYYVDGNTLSPENCPEVLYLMLRCLWS 840  
QY 841 KLPADRPSEFTSIRHILERMCEAECTVSV 869  
DB 841 KLPADRPSEFTSIRHILERMCEAECTVSV 869  
QY 868 KLPADRPSEFTSIRHILERMCEAECTVSV 868  
DB 868 KLPADRPSEFTSIRHILERMCEAECTVSV 868

RESULT 4  
US-09-974-298-129  
Sequence 129, Application US/09974298  
Patent No. US20020156263A1

GENERAL INFORMATION:  
APPLICANT: Chen, Huel-Me1  
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER  
FILE REFERENCE: PA-0037 P  
CURRENT APPLICATION NUMBER: US/09/974,298  
CURRENT FILING DATE: 2001-10-04  
PRIOR APPLICATION NUMBER: 60/238,331  
PRIOR FILING DATE: 2000-05-10  
NUMBER OF SEQ ID NOS: 194  
SOFTWARE: PERL Program  
SEQ ID NO 129  
LENGTH: 937  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc-feature  
OTHER INFORMATION: Incyte ID No. US20020156263A1 1331526CD1  
US-09-974-298-129

Query Match 19.7% Score 899; DB 9; Length 937;  
Best Local Similarity 31.5%; Pred. No. 2.4e-45;  
Matches 229; Conservative 102; Mismatches 254; Indels 142; Gaps 20;

QY 221 HNYT--FGSEVTLHCTATGIPVPTIWIENGNAVSSGSIQESVKDRVIDSRLO--LEFT 275  
DB 65 NNITSLGQTAELHCKVSGNPPPIIRKFKNDAPVQPRRLSTRSTYGSRLRIKRLDIT 124  
QY 276 KGLIYCIATNKGKSTAKAATLSIAEMSKP---QKDNKGCAOYRGECVCAVLAK 331  
DB 125 DTGFCVAVANKEVSVSTGLVFKFGPPPTASFGYDEVEDGFCQPYRGIAAC-ARFIG 183  
QY 332 DALVFLNTSYADE-EOELLVHTAMLEKLVSPVPCRAAEALCNHIFQEC-SPGVPT 389  
DB 184 NRYVMSLSHMOEIEQITAAFTYCTSSHLSDKSGFAPISLCHAFYCOETSSVPK 243  
QY 390 PIPCREYCLAVKELCAKEMLVMEKTHRGLYRSE--NHLVSPKSKLPMSHMDPTA 446  
DB 244 PDLRCRDECEILNVLCOYEYI-----FARNPMILMLRLKLPNCEDLPQESPEEA 294  
QY 447 -CAR--LPHLDYKKNKTF-----PMTSSKPSV----- 473  
DB 295 NCTRIGIPMADPINKNKKCYNSTGVDRGTAVSVTKSGROQCPNNSQVPHHTFTALNFE 354  
QY 474 -----DIPNLSSSSSFSVSPYTMVTIISIM 501  
DB 355 LNGTHSVCRNPGNOKEAPMCFITDENFKSDLCIDIPACDSKDSKKN-----KHEILYIV 409  
QY 502 SFAIFVLTITLTYCCRRKQKNNKRESAAVTLTLPSELLDRLHPNMYQMP--- 558  
DB 410 PSVAIPALALFEFTCVCR--NNOKSSSAPV-----QRPKHV 446  
QY 559 -----LLLN-----PILLSLEYPRNNIEYRDIGGAFGRVQARAPGLLPY 606  
DB 447 RGVNEMSMINAKPKSKAEPLSAVREMEELGECAFGLYGHLYLTPM---DHAOLV 503  
QY 607 AVMLKEASADQADQOREALMAEFDPNPIYKLVCAVKGKPMCLFEYMAVGLNEF 666  
DB 504 AILKTLDDYNNPQOMMEFOQASLMAELHNPVICYLGATYQDEPVCMLTEFYINQGLDHEF 563  
QY 667 LRSMSPHYVCSLSHSDLSMRQVSSPPPLSCAEOLCIAROVAAGMAYLSERK 726  
DB 564 LMRSP-----HSDVGCSSDEDTGVKSSLDHGFELHIAIQTAAEMEYLSHFVHKDL 616  
QY 727 ATRNCLVGENNVYKIAFGLSRNTYSADYKANEANDAIPRMPPEISIFNRYTSSDW 786  
DB 617 AARNIILGEOHAKYISDLGSLREITSADYRVOSKSLPTRMPPEALINYGKSSSDITL 676  
QY 787 AYGVLMEITSYGLQYRYGMAHEVITYYVDGNTLSPENCPEVLYLMLRCLWSKLPADR 846  
DB 677 SFGVVLMEITSYGLQYRYGMAHEVITYYVDGNTLSPENCPEVLYLMLRCLWSKLPADR 846  
QY 847 PSFTSIH 853  
DB 847 PSFTSIH 853



[illegible]

RESULT 7  
 US-09-966-147--9  
 : Sequence 9, Application US/09966147  
 : Patent No. US20020146416a1  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Presta, Leonard G.  
 :               Shelton, David L.  
 :  
 :               Urfer, Roman  
 :  
 : TITLE OF INVENTION: HUMAN TRK RECEPTORS AND NEUROTROPHIC FACTOR INHIBITORS  
 :  
 : NUMBER OF SEQUENCES: 41  
 :  
 : CORRESPONDENCE ADDRESS:  
 :               ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP  
 :               STREET: 620 Newport Center Drive, 16th Floor  
 :               CITY: Newport Beach  
 :               STATE: California

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? COUNTRY: USA
? ZIP: 92660
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: WinPatIn (Genentech)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/966,147
? FILING DATE: 27-Sep-2000
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/446172
? FILING DATE: 19-MAY-1995
? APPLICATION NUMBER: 08/286846
? FILING DATE: 05-AUG-1994
? APPLICATION NUMBER: 08/215139
? FILING DATE: 18-MAR-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Dreger, Ginger
? REGISTRATION NUMBER: 33,055
? REFERENCE/DOCKET NUMBER: GENENT. 33CP04C
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 954-4114
? TELEFAX: (415) 954-4111
? INFORMATION FOR SEQ ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 790 amino acids
? TYPE: Amino Acid
? TOPOLOGY: Linear
? SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-966-147-9

Query Match 17.7%; Score 810; DB 10; Length 790;
Best Local Similarity 27.4%; Pred. No. 3,6e-40;
Matches 255; Conservative 116; Mismatches 256; Indels 304; Gaps 30

QY 1 MRELNIPIVLVILTV-----ARSGTEKLPKAVITTPLETVDAIVEAVTFMKA 50
DB 84 LRDRLGELNRLITVKSGLRFPVADAHNFRRLSRMLSEFNALS----- 129
QY 51 VESYQPEISWTNRKKILIKLEDTRYISIRENGQLTILSVESDDGICSTA-----N 102
DB 130 -----LSW-----KTVQGLSDLELVLSGNRLHSCALRMILQWREE 164
QY 103 NGVGGAYE-----SCALQYKMKPKITRPPIVINKIIEGLKAVLCPTTM 145
DB 165 EGLGVEPEQKLOCHGQGRPLAMPNAPSVCVPTLKQVY-----NASVUGDDVLRLQVE 218
QY 146 GNPFRYSWMIGDSDPLRENSRIA-VLESG-----SLRIHNYQKE-DAGQYRCVAAKNSLGT 198
DB 219 GRGLEQAGWT-----LTELQSAIVYKMSGGLPSGLGLTANVTSIDLNRKLTQMAENDVGR 273
QY 199 AYSKVYKLEFEVFARILRAPESHNVTEGSEFYLH-----C-----TATGIVPPIITME 247
DB 274 A-----EVSQYV-----NVSFPAVSQVLIHVAEMHNHMCIFPSVDGQPARBLRYLF 317
QY 248 NGNAVSSGS-----IQESVADRYIDSKLOFLTKP-----GLYTICIAITKNHGEKFEJAK 296
DB 318 NGSVLNIETSEFTFELBPAANEYTRHGCLRL-NQPTVHNVNGNYTLLLANPFGQ----- 369
QY 297 AAATISIAEMSKPKQDNKGYCAQYRGVEYCNVLAIKDALVLFNTSVADDEEBOELLVHTAW 356
DB 370 ASASIMAAFMNPFEPN-----PEDPLPTDNTSISGDVEKND----- 406
QY 357 NELKVVSPVCRPAEALLCNHIFQEGSPGVVPTPIRLICREYCALVELKESAKEMWLWEEK 416
DB 407 -----EPFGVAVAGLAV-PAC----- 423
QY 417 THRGLYSEMHLLSVPCSKILRSMHMDPTACARLPHLDYKNEMLKTPRPMTSKPSVDIP 476
DB 424 -----LFLVSTL-LVLIANKGR-----RNFFGI-----NRPAVLAP 452

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QY 477 NLPSSSSSF-----SVPTYSMTVIISIMSSFAIVLLTTTLTYCCRRRQMKKRE 530
DB 453 EDGLAMSLFPMILGSSLSPTG----- 475
QY 531 SAAVTLTLPSELLDRHPNPNYQRMPLLPKLLSLEYPRNNIEYVNDIGEGAGRYE 590
DB 476 -----KSGLOGHIENPOYFSDACVHHK-----RDIYLMKELEBGAAGRYE 519
QY 591 QARAPGLPEPFTVAVMKLEASADQADFOREALMAEFNDPNYKLLGVCAVGRP 650
DB 520 LAECNHLPEODKMLVAVAKLK-EASESARODFOREALMLTMOHOHIYRFGVCEGRP 578
QY 651 MCLLEFYMAVGDLEFLRSMSPHTVCSLSHDSLSMAQVSSGPPPLSCAEOICIAROYA 710
DB 579 LLMVFEYMRHGDNLRLRSHGP-----DAKLAGEEDVAPGPIGLGOLAVASQYA 629
QY 711 AGMAVSEKFEYHRDLATNCLVGENMVKIADFGSRNITYSADYKANENDAIPIRMP 770
DB 630 AGMAYLAGLHFVHRDLATNCLVGOGLVYKIGDFGSRDIYSTDYRVGGRMLPIRMP 689
QY 771 PESIFNRYTTESDVAWGVVMEIFSYGLOPYGNAHEVYIYVDGNILSCPENCPYE 830
DB 690 PESILYRKFTTESDVMSFGVYLMETFTYKOPWYOLSNTEALDCTIYGELERPRACPE 749
QY 831 LYMMLRCLWSKLPADRPSTSIHRILERCE 861
DB 750 VYAIMRCWQREPOQRHSIKDVHARLQALAQ 780

```

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RESULT 8
US-09-924-859A-3
; Sequence 3, Application US/09924859A
; Patent No. US20020137113A1
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Sadick, Michael D.
; APPLICANT: Shelton, David L.
; APPLICANT: Wong, Wei Lee Tan
; TITLE OF INVENTION: KINASE RECEPTOR ACTIVATION ASSAY
; FILE REFERENCE: P0854CIP2C1
; CURRENT APPLICATION NUMBER: US/09/924, 859A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US/09/417, 381
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 3
; LENGTH: 814
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-924-859A-3

```

```

Query Match 17.7%; Score 810; DB 10; Length 814;
Best Local Similarity 27.4%; Pred. No. 3, 8e-40;
Matches 255; Conservative 116; Mismatches 256; Indels 304; Gaps 30;

QY 1 MRELVINPLVHILTY-----AFSGTEKLPKAPVITPLETVDALEEVAAEFMCA 50
DB 108 LRLDLRGELRLNLTIVYSGLRFAVADPAFHPTPLRSLNLSFNALSS----- 153
QY 51 VESTIPEPEISWTNRKILKFLDRYRSIRENGQLITISVSDSDGIIYCTA-----N 102
DB 154 -----LSW-----KTVQGISLOELVLSGPHLSCALRMLOWEE 188
QY 103 NGVGAWE-----SCGALOVKMKPRITPRPINVKIIEGILKAVLPCTM 145
DB 189 EGIAGVPEQKLOCHGQOPPLAHMRAASGVPTLKVQV-----NASVDVDDVILRQVE 242
QY 146 GNPFPYSWIKGDSPLRENSRIA-VLESG-----SLRHHVQRE-DAGYRCVAKNSLGT 198
DB 243 GRGLEQAGWI-----LTLEBSATVMSKSGGLPSIGLAVTSDLNKRLTCAWENDVGR 297
QY 199 AYSKYVLEFEVFAIRILRAESHNVITGSEVTLH-----C-----TATGIPVTIWI 247

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DB 298 A-----EVSVOY-----NVSFASVGLHVAENHHCIFPSVDGQAPSLRMLF 341
QY 248 NGNAVSGS-----IQESKRVIDSRLQLEFTRP-----GLYCIATNKGEEFSTAK 296
DB 342 NGSVLTNETSFITEFELEPANETVRHGLRLT--NPTHVNNQNTYLLANPFGQ----- 393
QY 297 AAATISIAEMSKPQDNKCYCAQYGEVCNAVLADELFLNTSYADPEAOELLVHTRAM 356
DB 394 ASASTIAAEMDNPEFN-----PEDPIIDTNTSGDPEKKD 430
QY 357 NELKVSPYCRPAEALCNHIFQCSGPGVPTPIPICREYGLAVKELECANEMLWEEK 416
DB 431 -----ETPGVSAVGLAV--FAC----- 447
QY 417 THRGLYRSEMHLLSVKCKSKLPMSHMDPFRACARLPHLDYKNKNLTFPMPTSSKPSYDIP 476
DB 448 -----LFLSTL-LLVNKKGR-----RNKRGF-----NRPAVLAP 476
QY 477 NLPSSSSSF-----SVPTYSMTVIISIMSSFAIVLLTTTLTYCCRRRQMKKRE 530
DB 477 EDGLAMSLFPMILGSSLSPTG----- 499
QY 531 SAAVTLTLPSELLDRHPNPNYQRMPLLPKLLSLEYPRNNIEYVNDIGEGAGRYE 590
DB 500 -----KSGLOGHIENPOYFSDACVHHK-----RDIYLMKELEBGAAGRYE 543
QY 591 QARAPGLPEPFTVAVMKLEASADQADFOREALMAEFNDPNYKLLGVCAVGRP 650
DB 544 LAECNHLPEODKMLVAVAKLK-EASESARODFOREALMLTMOHOHIYRFGVCEGRP 602
QY 651 MCLLEFYMAVGDLEFLRSMSPHTVCSLSHDSLSMAQVSSGPPPLSCAEOICIAROYA 710
DB 603 LLMVFEYMRHGDNLRLRSHGP-----DAKLAGEEDVAPGPIGLGOLAVASQYA 653
QY 711 AGMAVSEKFEYHRDLATNCLVGENMVKIADFGSRNITYSADYKANENDAIPIRMP 770
DB 654 AGMAYLAGLHFVHRDLATNCLVGOGLVYKIGDFGSRDIYSTDYRVGGRMLPIRMP 713
QY 771 PESIFNRYTTESDVAWGVVMEIFSYGLOPYGNAHEVYIYVDGNILSCPENCPYE 830
DB 714 PESILYRKFTTESDVMSFGVYLMETFTYKOPWYOLSNTEALDCTIYGELERPRACPE 773
QY 831 LYMMLRCLWSKLPADRPSTSIHRILERCE 861
DB 774 VYAIMRCWQREPOQRHSIKDVHARLQALAQ 804

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RESULT 9
US-09-924-859A-7
; Sequence 7, Application US/09924859A
; Patent No. US20020137113A1
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Sadick, Michael D.
; APPLICANT: Shelton, David L.
; APPLICANT: Wong, Wei Lee Tan
; TITLE OF INVENTION: KINASE RECEPTOR ACTIVATION ASSAY
; FILE REFERENCE: P0854CIP2C1
; CURRENT APPLICATION NUMBER: US/09/924, 859A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US/09/417, 381
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 7
; LENGTH: 850
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-924-859A-7
Query Match 17.7%; Score 807.5; DB 10; Length 850;
Best Local Similarity 26.1%; Pred. No. 5, 6e-40;

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Matches 252; Conservative 125; Mismatches 246; Indels 343; Gaps 36;

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QY 6 NIPLVHI-----LFLVAFSGTEKL-----PKAPVITTTLEFVDALVEE 43
Db 104 NITSIHENRSLHTLNAVDMELTYGLQKLTINKSGLRSTQPRFAKPNPLRYINLSSNR 163
QY 44 VAFMCAVESYPOPEISWTNRKLIKLFDRYSIRENGQLTTLISVED-----91
Db 164 LTT-----LSM-----QLFQT-LSLRE-----LQLQNFNCSCDIRMM 196
QY 92 -----SDDGITCCCTAANNVGGA-----VESCGLAQVKKPKITRPPIVKI 132
Db 197 QLMQEOGEAKLNSQNLICINAD-----GSQPLFRMNTSQCDL-----PEISVSHVLTIV 246
QY 133 IEGKAVLPCTTGNPNKPSYSWI-----KQDSPLRNSRIAVLESGSLRHNVOKEDEG-Q 187
Db 247 REGDNNAVITCNGSSPLPDVDMIVTGQSINTHOTNLNMTNVAINLTLNVTSEDNGFT 306
QY 188 YRCVAKNSLG-----TAY--SKYVKLEFEVFAIRILRAPE--SHNVTGSEFVTLHCT 234
Db 307 LFTCIAENVVGMNSNAVALTYYPFRVYSLE-----EPBLRLHCHIEF-----V 349
QY 235 ATGIPVPTTIWINGNAVSSGST--QESVADRVIDSRLQLEFTRP-----GLYTCTATNK 287
Db 350 VRGNPPTLHMLHNGQPLRESKLIHVEYIOGEISEGCLLF--NKPTHYNGNNTLLAKNP 408
QY 288 HGEKSTAKAAATISIAEMSKPKDNKGYCAQYRGECVNCNVLAKDALVPLNTSYADEEA 347
Db 409 LG-----TANQITIN-----GH-----FLKEPP--PEST 429
QY 348 QELLVHTANMELKVVSPVCRPAEALLCNHIFQECSPGVPTPIPICREYCLAVKELCA 407
Db 430 DNF-----LFDEVSP-----440
QY 408 KENLVMEKTHRGIRSEMHLLSVPKSKLPSMHNMDPTACARLPHLDYKNENKLTFRPMT 467
Db 441 -----TPPIIT 445
QY 468 -SSKPSVDIPNLPSSSSFSVSPTYSMTVYISMSFAJFVLLTTTLVCCRRRKQMN 526
Db 446 VTHKPREED-----TFGVSTAVGLAACVLLVLFPMINKYGRSRFGM 489
QY 527 K-----KRESAAVTL-----TTLPSSELLDLRLHPNM--YORNPLLNPKLSLEY 570
Db 490 KGEVAIVISGEDSASPLHINHGITTPSSL--DAGPDVYVIGTRIPVLENPQYFNGH 546
QY 571 -----PRNNEYVRDICEGAFGRVFOARAGLPIPEFTVVAVKMLKEASAD 618
Db 547 NCHKPPTYOHIKRDIYVLRKEGEGAFKVFIAECYNLSPTKDKMLVAVALKADPTLA 605
QY 619 MQADFOREALMAEFDPNIVKLLGYCAVGKPMCLLEFYMAVGDNLFEFLSMSPPHTVCSL 678
Db 606 ARKDGDFQEAELNLNQHNEHIVKFGYCGDGDPLIMVEFYMKHGDNLNFKLAHGP 660
QY 679 SHSDLSRAQVSSBPP-----PLSCAEOLCIARQVAAGAAVYLSERKFVRDLATNCLV 733
Db 661 -----AMILVDGQPRQAKGELGSLQMLHIASQIASGMVYLASQHFVARDLATNCLV 712
QY 734 GENNVVYIADFGSLRNYSADYKANKENDAIPIRMMPRESIFRNRYTSEDVWAGYVLM 793
Db 713 GALLLVKIGDFGMSRDVYSTDYTRVGCHTMLPIRMMPRESIMRKFTESDVWSPFGVILM 772
QY 794 EIFSGLQPYGYGAHEEVIYVBDGNLTSCPCNPVELYINLMRLCSKLRPADRPSFSIH 853
Db 773 EIFTYGGKQWFOLESNTEVICITQGRVLEBRVCPKEVYDVMLGCMQREPOQRLNKEIY 832
QY 854 RILERM 859
Db 833 KILHAL 838

```

RESULT 10  
US-09-966-147-6

Sequence 6, Application US/09966147

Patent No. US20020146416A1

GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.

Urfer, Roman

Shelton, David L.

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Shelton, David L.

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QY 288 HGEKSTAKRAATISTAEMSKPOKDNKGCAOYRGEVCNAVLAADALVPLINTSYADPEEA 347
DB 384 LG-----TANOTIN-----GH-----FLKEPF--PEST 404
QY 348 QELLVHTAMNELKVSPVCPRAAEALLCNHIFQESGCVVPTPIQREYCLAWEKELCA 407
DB 405 DNFI-----LDFEVS----- 415
QY 408 KEMLVMEKTHRGLYNSEHMLLSVPCSKLPSMHMDPTACARLPHLDYKENTKTPPPMT 467
DB 416 -----TPPI 420
QY 468 -SSKSPVDIPNLPSSSSSSSVSPYSMTYIISMSFAIFVLLITTLCCRRKMKWN 526
DB 421 VTKRPEB-----TFGVSTAAGLAFAVLLVFLVMKRYGRSKFGM 464
QY 527 K-----KRESAAYTL-----TTLPSLELLDLRHPNPM--YORPPLLNLKLSLEY 570
DB 465 KGVAVVAGSEDSASPLHHINHGITPPSSL--DAGDVIYIGMTIRIPVIEPNQYFRQGH 521
QY 571 -----PRNNIEYVRDIEGAFGVFOARAGLLPPEFTVNAVKMLKEASAD 618
DB 522 NCHRPPTYOYHKKRIVLKLRELGEAFGVFLAECYNLSPTKDKMLVAVALKADPTLA- 580
QY 619 MOADFOREALMAEFDPNPIVTKLLGCAVGRPMCLLFETVYAGDLNEFLRSMSPHYCSL 678
DB 581 ARDPQREALLNLNCHIEHIVKRYGVCGDDPLIMVEYKHKDINKLELAHGP----- 635
QY 679 SHSDLSMRAQVSSPPGP-----PLSCAEOLCIARQVAAAGVYSEKFEVHRDLATNCLV 733
DB 636 -----AMILVDGQPRQAKGELGSLQMLHIASQVGYLASQHFVHRDLATNCLV 687
QY 734 GEMVYVIAFGISRNITSADYK--ANEND-----AIPRMPSPSIFENRY 779
DB 688 GANLVLKIGFGSRDYSTDYTRLPNSGNDPCIMCEVGHMLPIRMPPEISIMYKRF 747
QY 780 TTESDVAWYGVLMIEFSYGLQPYGMAHEVITYYRDGNILSCPENCPELYNLMELCW 839
DB 748 TTESDVAWVFGVILMEIFYTGKQPMFQJLSNTEVIECTIQGVLEBRVYCPREYDVMLGCW 807
QY 840 SKLPADRPSTSTHRIIERM 859
DB 808 QREPOQRLNKEITYKILHAL 827

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RESULT 11  
US-09-961-403-3

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; Sequence 3, Application US/09961403
; Publication No. US20030077589A1
; GENERAL INFORMATION:
; APPLICANT: HE-STUMP, HOLGER
; APPLICANT: HAENDLER, BERNARD
; APPLICANT: KRAETZSCHMAR, JOERN
; APPLICANT: KREFT, BERTHOLD
; APPLICANT: WINTERHAAGER, ELKE
; APPLICANT: REGIDOR, PEDRO
; APPLICANT: SCOTT, SIMONE
; TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
; FILE REFERENCE: SCH-1789
; CURRENT APPLICATION NUMBER: US/09/961.403
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1070
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-961-403-3

```

Query Match 16.9%; Score 774; DB 9; Length 1070;  
Best Local Similarity 27.2%; Pred. No. 6.9e-38;  
Matches 228; Conservative 137; Mismatches 304; Indels 168; Gaps 29;

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QY 55 POEISMTNKLILIKLFDTRYISIRENGOLITLIVESDDGICYCTANNVGGAVERSCGA 114
DB 350 PEPVSMHEAGVLA---PTHGRRYQKGHELYLVANLIESDAGYTTGHAANLACGRDVA- 405
QY 115 LQYKMKRITTPRINVKIIEGLKAVLPCTMGNPKSVSWIKGDSPLRENSRIAVLESGS 174
DB 406 ITVAIVPSMLKRPQDSQLEEGKPGYDLQATPKPTVWYRQMLISDSREYEVKNGT 465
QY 175 LRHNQKEDAGQRCVAAKNSLGTASKYVYKLEFEVAFARLRP---ESHNTYFGSFVTL 231
DB 466 LRINSVEYDGTWYRQMSSTPAGISIAQAA--LQVLEKLTFTPPPOQCMGFDEATV 522
QY 232 HCATGAPVPTIWIENGNAVSSGSIQESYKDRVIDISRLQLFITK-----PGLYTCIATN 286
DB 523 PCSATGREKPTIMER-----ADGS---SLPEVNTNAGLHARVTRDAGNYCTIASN 574
QY 287 KHGEKSTAKAAATISTAEMSKPOKDNKGCAOYRGEVCNAVLAADALVPLINTSYADPEE 346
DB 575 -----GPOGQIRAHVOLTV-----AVFI--TEKVEPER 600
QY 347 AOELLVHTAMNELKVSPVCPRAAEALLCNHIFQESGCVVPTPIQREYCLAWEKELC 406
DB 601 TTVYQGHYA-----LQCEAOGDPKPL----- 622
QY 407 AKEMLVMEKTHRGLYNSEHMLLSVPCSKLPSMH-----WDPTACARLPHLDY 455
DB 623 -IQW-----KGRKRLDPKRLG--PRNHIFQNSGLVHDAVEDSGRYCIAG 667
QY 456 KNEMLK-TTPPPMTSSKRPVDIPMLPSSSSSESVSPYSM--TVIISMSFAIFVLLTI 512
DB 668 NSCNIRKHTAPLY---VVDKP--VPSESEGPS--PPYKMIQTIGLSVGAAYVITYIAVVG 721
QY 513 TLYYC---CRRKMKKRESAAYTL-----TTLPSLELLDLRHPNPMYORM 557
DB 722 LMFTCKKRCARLQOPBESEPEMCLNGPIQNOPSAIEQVAVLISLGGPATNK 781
QY 558 PLLNPKLSLEYPRNNIEYVRDIEGAGRGVFOARAGLLPPEFTVNAVKMLKEASA 617
DB 782 RHSTSDK---MHPRSSIOPITTLGKSEFEVFLAAGQIEGVAETLVLYKLSQSK-DE 837
QY 618 DMQADQREALMAEFDPNPIVTKLLGCAVGRPMCLLFETVYAGDLNEFLRSMSPHYCS 677
DB 838 QQQDLFERLEMGKLVHANVRLGLCPRAEETHVLEVDLEDLKQFIR----- 888
QY 678 LSHS-DLSMRAQVSSPPGPPLSCAEOLCIARQVAAAGVYSEKFEVHRDLATNCLVGEN 736
DB 889 ISKSKDEKLKSQ-----PLSTKQKVALCTOYALGMEHLSNNRFVHKDLAARNCLVSAQ 941
QY 737 MYVKIADFGISRNITSADYKANDENAIPIRMPPEISIFYKRTTSDVAWYGVLMIEIF 796
DB 942 ROYKVSALIGLSKVYNSYEHFRO--AMVALRMAWSPPEALLEGDSTSDVAWVAGVLMWVEV 1000
QY 797 SYGLQPYGMAHEVITYYRDGNI--LSCPENCPELYNLMRLKMSKLPADRPSTST 852
DB 1001 THBMPHGGQADDEVLDLADGAKARLPQBPCCSKLYRLMQRMALSPKDRPFSSEI 1057

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RESULT 12  
US-10-242-943-4

```

; Sequence 4, Application US/10242943
; Publication No. US20030087412A1
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Schulz, Vincent P.
; APPLICANT: Yang, Melja
; TITLE OF INVENTION: NIK1 PROTEIN AND NIK1 PROTEIN COMPLEXES
; FILE REFERENCE: 15966-521 NIK1 protein complexes
; CURRENT APPLICATION NUMBER: US/10/242.943
; PRIOR APPLICATION NUMBER: US/09/167,206
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 26

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SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 4  
 LENGTH: 641  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-242-943-4

Query Match 16.2% Score 741; DB 9; Length 641;  
 Best Local Similarity 36.5%; Pred. No. 3.5e-36;  
 Matches 183; Conservative 70; Mismatches 159; Indels 90; Gaps 14;

QY 394 CREY-----CLAVELFCARWMLMEKTHRGVLRSEMHLLSVPKSKLPSMH 441  
 DB 154 CREMDEQIRLMDQMLKCLSAE-----EKYSQKEDK-----YEEIKITL-----DKL--- 197  
 DB 442 WDFPACARLPHLDNKNELKTFPPMTSSKPSVDLPNCPSSSSSFVSPTYSMTV-IST 500  
 DB 198 -----EAEFRAEFARSVAKLEKTDLEDNNTSGDPVEKKDETPFGVSV 243  
 QY 501 MSSEFAIVLLITTLTY-----CCRRRKQMKNK-----KRESAAYTL-----TTLPSE 542  
 DB 244 AVGLAVFACLEFLSTLLVANKGRNKFGINRPAVLAPEDGLAMSLHFMILGSSLSPT 303  
 QY 543 -----LLIDRLHPNPMYQMPILLNPKLLSLEYPPNNIEYVADIGEGAFGRVFOARAGLT 598  
 DB 304 GKSGSLGHIENFQYFSDACVHHIK-----RRDIYKLWELGEGAFKGVFLAECHNLL 356  
 QY 599 PYEFTWAVYKMLKEASADQADFOREALMAFEQNPNTYKLLVCACVCKPMLLEFYM 658  
 DB 357 PEQKMLVAVKAL-ESASARQDFORAEELTLMLOHIVRFQVCTEGPPLMVEYM 415  
 QY 659 AYGDNLNFKRMSPHYVCSLSHSDLSRAQVSSPGPPLSCAEQLCIARQVAAAGVASE 718  
 DB 416 RHGDLNFRLSHSG-----DAKLLAGEEDVAPPLIGLIGLAAVSAQAAQVAVYLR 466  
 QY 719 RKFYHRLATRNCLVGENMYKTAQFGLSRNITSADYKANKENDALPIRMPPESITYNR 778  
 DB 467 LHFHRLATRNCLVGENMYKTAQFGLSRNITSADYKANKENDALPIRMPPESITYNR 778  
 QY 779 YTFESDWAYGVVLMLEFSGLOPYGYMAHEVEVYVRDGNILSCPNCPVELYNLRLC 838  
 DB 527 FTTESDWAYGVVLMLEFSGLOPYGYMAHEVEVYVRDGNILSCPNCPVELYNLRLC 838  
 QY 839 WSKLPADRPSTSIHRLERMC 860  
 DB 587 MOREPSNATA-----SRMC 600

RESULT 13  
 US-10-011-548-33  
 Sequence 33, Application US/10011548  
 Publication No. US20030055218A1  
 GENERAL INFORMATION:

APPLICANT: Timans, Jacqueline C.  
 Antonius  
 Sana, Theodore R.  
 Bazan, J. Fernando  
 Kastelein, Robert A.  
 TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and  
 Methods  
 NUMBER OF SEQUENCES: 36  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: DNAX Research Institute  
 STREET: 901 California Avenue  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/011,548  
 FILING DATE: 22-Oct-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/173,151  
 FILING DATE: <unknown>  
 APPLICATION NUMBER: US 60/065,776  
 FILING DATE: 17-Nov-1997  
 APPLICATION NUMBER: US 60/078,008  
 FILING DATE: 12-Mar-1998  
 APPLICATION NUMBER: US 60/081,883  
 FILING DATE: 15-Apr-1998  
 APPLICATION NUMBER: US 60/095,987  
 FILING DATE: 10-Aug-1998  
 APPLICATION NUMBER: US 60/078,416  
 FILING DATE: 18-Mar-1998  
 APPLICATION NUMBER: US 60/062,066  
 FILING DATE: 15-Oct-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Chung, Edwin P.  
 REGISTRATION NUMBER: 34,090  
 REFERENCE/DOCKET NUMBER: DX0767X  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650)852-9196  
 TELEFAX: (650)496-1200

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 802 amino acids

TYPE: amino acid

STRANDEDNESS: No. US20030055218A1 Relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-10-011-548-33

Query Match

Best Local Similarity

Matches 230; Conservative 104; Mismatches 266; Indels 237; Gaps 27;

QY 84 LTLISVEDSDGIGYCCTANNV-----GGAVESGALQYKMKRTTRPEIN---- 129  
 DB 86 LEIASFLPEDAGRILCLARGSMIVLQNLTLITGSLTSMNDE---DPKSHRDSNNHSY 142  
 QY 130 -----VKITEGLKAY-----LPCTMGNPKPSYWIKGDSPLEKNSRIAVL-- 170  
 DB 143 PQQAPYTHPQRMREKTLHAAVPAAGNTYKRCFPAAGNPTPIRMLKDGAFGENNIGIRL 202  
 QY 171 -ESGSLRHHNQKEDAGYRCVAKNSLGT-AVSKYVK-LEFEVFARILRA--PESHNVT 224  
 DB 203 RHQWMSLYMSVPSDGGITTCLEAVNAVGSIIRNIVLDVLEERSHRIITLQGLPANTTAV 262  
 QY 225 FGSFVTLCTATGIPVETITWIE---NGN---AVSSGSIOESYKDRVIDSRQLQFTTK- 276  
 DB 263 VGSVVELLCKYSDAQPHIQMLKHIYINGSSFGVGPYQVLTADINSSEVEVLYLRN 322  
 QY 277 -----PGLYTCIATNKHGEKFSRAKAAATISIAEMSK--POKNGKGCAYRGEVCNAV 329  
 DB 323 VSAEDAGEYTCLAGNSIGLSYQSA-----WLTVLEEDPTWTAAPPEARVYDIL 372  
 QY 330 AKDALVELNTSYADPEAEOLLYHTAVNELKVVSPVCPAAEALLCNHIFQECSPGVVPT 389  
 DB 373 -----YASGSLALAVLLLLA----- 387  
 QY 390 PIPICREYCLAVKELFCARWMLMEKTHRGVLRSEMHLLSVPKSKLPSMHMDPTACAR 449  
 DB 388 -----GLRGC-----ALH-----GR 398  
 QY 450 LPHLDYKKNELKTFPPMTSSK-----PSVDLPNCPSSSSSFVSPTYSMTVSISSSFA 505  
 DB 399 HPR-----PPATVOKLSRFPLARQFSLSSGSSGKSSSLVLRGV-----LSSSG 442

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QY 506 IFVLLITTLTTCORRRKMKKRESAAVLTTLTLPSELILLDRHPNMYORMLLNPKL 565
DB 443 PDLMLGLVSL-----DLPID-----PLM-----460
QY 566 LSLFPRNNIEYVRDIEGAFGRVFOARAPGLLPER--FTWAVKMLKEASADMOADE 623
DB 461 ---EPRDRLVKPLGEGCGGVVRAEAFGMDPARPOASTVAVKMLKDNASDKDLADL 517
QY 624 QREAAALMAEFD-NPNIVKLLGCAVAKPMLCFEYVAYGDLNFEFLASMSHTYCSLSHD 662
DB 518 VSEMEVWKILGRKRNILINLGVCTQEGPPLYIVECAKAGNLREFLRARP-----PGPD 571
QY 683 LSRMAOVSSPPPLSCAEQICIAQVAAAGMAYLSRKFVRDLATRNCLVGENMYVYKIA 742
DB 572 LSPDGRSSBG--PLSFPLVSCAYQVARGMOLLESKRCIHRDLARNVLTEDNWKIA 629
QY 743 DGLSNRIYSADYKANKENDALPIRMMPRESIFYNRYTTESDWAYGVVLMELFISYGLP 802
DB 630 DGLAGVHHIDYKKTSGNRLPVKMAPEALFDRVYTHQSDVMSGILLMEIFTLGGSP 689
QY 803 YYGMAHEVYIYVRDNIILSCPNCVELYNLMRLCWSKLIPADRPSTSIHRLERN 859
DB 690 YPGIPEELFSLLRGHRMDRPHCPPELYGLMRECMHAAPSOQRPFKOLVEALDXY 746

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RESULT 14  
US-09-758-386-3

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; Sequence 3, Application US/09758386
; Patent No. US20010016355A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-5
; FILE REFERENCE: PF486PCT
; CURRENT APPLICATION NUMBER: US/09/758,386
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/293,182
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-758-386-3

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Query Match 15.2%; Score 693.5; DB 10; Length 802;  
Best Local Similarity 27.3%; Pred. No. 2.9e-33;  
Matches 243; Conservative 101; Mismatches 284; Indels 261; Gaps 31;

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QY 81 GOLLT-----ILSEVSDGIIYCCITANNNGVAGVESGALQVAKPKRTTPPINVKIIEG 135
DB 9 GVLLSVPGPVLSLEASSE-----VE-----LEPLASLSLEGQBEELVYALG 50
QY 136 LKAVLPCTWGNPKPSVSWIKGDSPLRENSRIAVLESGLRIINVOKEADAGYRCVAKNS 195
DB 51 QPVRLLCC--GRAERGGHMKESGRLAPAGRVGRWR-GRLEIASFLPEDAGRYLCLARGS 106
QY 196 -----LGTASKVYVKKLEFEVFAHLRAPESHN-----222
DB 107 MYVLQWLTLITGSLTSSNDE-----DPKSHRDBSNHSTPQAPYTHPQRMEKKL 139
QY 223 --VTFGSFYLIHCTATGIPVPTITWTENGNAVSS-----GSIQ-----ESVKDRVIDSRL 270
DB 160 HAVPAQNTVYKRCRPAQNPPTIRIWLKDGQAFHGENRIGIRLRHQMWSLVMSVYPS--217
QY 271 QLFITPGLYTCIAITKKGKSTAKAALITIAESKPOKD--NKGYCAQYGEVCNAV 328
DB 218 ----DRGYTCTIYENAVG---SIRYNLLDVLERS-PHRPILOGLIPAN-----TTAV 262
QY 329 LAKDALVPLNTSYADEAEQELLVHTAMN-----ELKVVSPVCRPAEALLCN 376
DB 263 VGSDD-VELLCKVYSDAQPHIQMLKHIVINGSFGADGFPYVOVLKADINSSEVEVLYLR 321

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QY 377 HIFQCSPGVVPPIPICRREY-CLAVKELECAKEMLMEEKTHRGYRSEMLLSVPKGS 435
DB 322 NVSAEDA-----GEYTLAAGNSI-----GLSYQSAWLTIVPE--353
QY 436 KLPDSMHDPYACARLPHLDYKNENLTFPPMTSSKPSVDIPNLPSSSSSSFVSPLYYSMT 495
DB 354 -----EDPMTAAAEARFT-----D369
QY 496 VIISIMSPALIFVLLITTLTTCORRRKMKKRESAAVLTTLTLPSELILLDRHPNMP--552
DB 370 IILYASGSLALAVLLIAGLY---NGQ-----ALHGHRPPRPAT 405
QY 553 --MYORMLPL-----LNPXLLS-----LEXPKN 573
DB 406 VOKLSRPLARQPSLESSSGSKSSSLRYRGVRLSSSGPALLAGVSLDPLDPLMEPRD 465
QY 574 NIEYVRDIEGAFGRVFOARAPGLLPER--FTWAVKMLKEASADMOADEFOREALMA 631
DB 466 RLVLGRLPLGEGCGGVVRAEAFGMDPARPOASTVAVKMLKDNASDKDLADLVSEMEVWK 525
QY 632 EFD-NPNIVKLLGCAVAKPMLCFEYVAYGDLNFEFLASMSHTYCSLSHDSLMSRAOVS 690
DB 526 LIGRHKNTIINLGVCTQEGPPLYIVECAKAGNLREFLRARP-----PGPDLSPOGRS 579
QY 691 SPGPPPLSCAEQICIAQVAAAGMAYLSRKFVRDLATRNCLVGENMYVYKIADEGLSRNI 750
DB 580 SEG--PLSFPLVSCAYQVARGMOLLESKRCIHRDLARNVLTEDNWKIADFGIARGV 637
QY 751 YSADYKANKENDALPIRMMPRESIFYNRYTTESDWAYGVVLMELFISYGLPYGMAHEE 810
DB 638 HHIDYKKTSGNRLPVKMAPEALFDRVYTHQSDVMSGILLMEIFTLGGSPYGLPVEE 697
QY 811 VIIVYVRDNIILSCPNCVELYNLMRLCWSKLIPADRPSTSIHRLERN 859
DB 698 LFSILRGHHRMDRPHCPPELYGLMRECMHAAPSOQRPFKOLVEALDXY 746

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RESULT 15  
US-09-757-415A-2

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; Sequence 2, Application US/09757415A
; Publication No. US20030040612A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Ming-Ming
; TITLE OF INVENTION: Methods of Identifying Modulators of the FGF Receptor
; FILE REFERENCE: 2459-1-002N
; CURRENT APPLICATION NUMBER: US/09/757,415A
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/175867
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-757-415A-2

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Query Match 14.9%; Score 679; DB 9; Length 822;  
Best Local Similarity 25.6%; Pred. No. 2.1e-32;  
Matches 231; Conservative 127; Mismatches 288; Indels 256; Gaps 30;

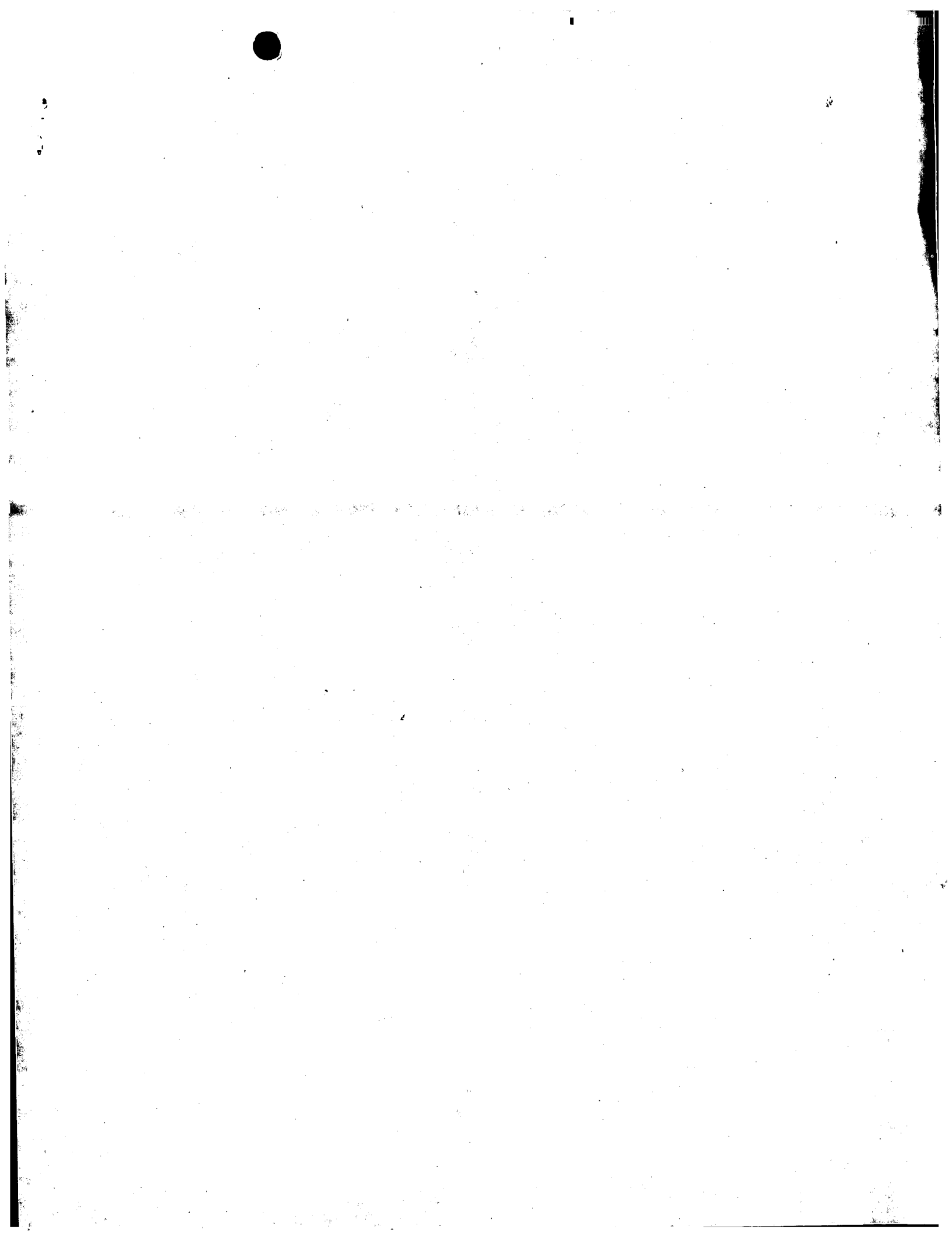
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QY 33 PLETVDAIVE-EVAFMCAVESTPOPEISWTRNKI-LILFPTRSIRNGOLLITLSV 89
DB 37 PVEVESLIVHPGDLLOLRCHRLDDVO-SINMLRDGVOLVESNRTRIIGE-----VEV 88
QY 90 EDS---DDGIYCTANNVG-----AVESGAL-----Q116
DB 89 RDSIPASGLYACTVSSPSGDTTYSVNVSDALPSEDDDDSSSEKEDNTKPKR 148
QY 117 VKMKPKITRPPIVWKIIEGLKAV---LPCTWGNPKPSVSWIKGDSPLRENSRIAYLE-171
DB 149 RPVAPVYTPSPKKKKKHAHAPAKYVFKPCSSGTPPTIRIWLKNGREFPDHRIIGYKV 208

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[illegible]

Search completed: June 18, 2003, 10:34:27  
Job time : 34 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2003, 10:21:12 ; Search time 18 Seconds  
(without alignments)  
1420.473 Million cell updates/sec

Title: US-09-817-487A-2

Perfect score: 4569

Sequence: 1 MRELVNIPVLHILTLVAFSG.....TSIRHLERMCERAGTVSV 869

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*

2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/1aa/PTCUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/1aa/Backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4558	99.8	869	1 US-08-374-834-16	Sequence 16, Appl
2	4558	99.8	869	2 US-08-644-271-29	Sequence 29, Appl
3	4558	99.8	869	4 US-09-077-955-33	Sequence 33, Appl
4	4292.5	93.9	868	1 US-08-374-834-1	Sequence 1, Appl
5	4292.5	93.9	868	2 US-08-644-271-1	Sequence 1, Appl
6	4292.5	93.9	868	4 US-09-077-955-1	Sequence 1, Appl
7	4269.5	93.4	868	5 PCT-US95-08493-21	Sequence 21, Appl
8	4220.5	92.4	860	5 PCT-US95-08493-19	Sequence 19, Appl
9	2897.5	56.9	530	5 PCT-US95-08493-13	Sequence 13, Appl
10	2597.5	50.6	478	5 PCT-US95-08493-2	Sequence 2, Appl
11	2312	50.6	478	5 PCT-US95-08493-15	Sequence 15, Appl
12	1577	34.5	304	2 US-08-701-191A-30	Sequence 30, Appl
13	899	19.7	937	2 US-08-469-537A-105	Sequence 105, App
14	876	19.2	943	2 US-08-469-537A-107	Sequence 107, App
15	862	18.9	821	1 US-08-339-578-2	Sequence 2, Appl
16	861	18.8	822	2 US-08-359-705B-2	Sequence 2, Appl
17	861	18.8	822	2 US-08-286-846A-2	Sequence 2, Appl
18	861	18.8	822	2 US-08-457-880A-2	Sequence 2, Appl
19	861	18.8	822	3 US-08-444-622A-2	Sequence 2, Appl
20	861	18.8	822	3 US-08-942-562-2	Sequence 2, Appl
21	861	18.8	822	4 US-09-156-923-2	Sequence 2, Appl
22	861	18.8	847	1 US-08-286-305A-5	Sequence 5, Appl
23	861	18.8	847	2 US-08-441-104A-5	Sequence 5, Appl
24	861	18.8	847	2 US-08-440-816A-5	Sequence 5, Appl
25	861	18.8	847	4 US-09-417-381A-5	Sequence 5, Appl
26	814.5	17.8	800	2 US-08-469-537A-72	Sequence 72, Appl
27	814.5	17.8	800	2 US-08-469-537A-78	Sequence 78, Appl

28	810	17.7	790	2 US-08-359-705B-9	Sequence 9, Appl
29	810	17.7	790	2 US-08-286-846A-9	Sequence 9, Appl
30	810	17.7	790	2 US-08-457-880A-9	Sequence 9, Appl
31	810	17.7	790	3 US-08-444-622A-9	Sequence 9, Appl
32	810	17.7	790	3 US-08-942-562-9	Sequence 9, Appl
33	810	17.7	790	4 US-09-156-923-9	Sequence 9, Appl
34	810	17.7	814	1 US-08-286-305A-3	Sequence 3, Appl
35	810	17.7	814	2 US-08-441-104A-3	Sequence 3, Appl
36	810	17.7	814	2 US-08-440-816A-3	Sequence 3, Appl
37	810	17.7	814	4 US-09-417-381A-3	Sequence 3, Appl
38	807.5	17.7	850	1 US-08-286-305A-7	Sequence 7, Appl
39	807.5	17.7	850	2 US-08-441-104A-7	Sequence 7, Appl
40	807.5	17.7	850	2 US-08-440-816A-7	Sequence 7, Appl
41	807.5	17.7	850	4 US-09-417-381A-7	Sequence 7, Appl
42	792.5	17.3	839	2 US-08-359-705B-6	Sequence 7, Appl
43	792.5	17.3	839	2 US-08-286-846A-6	Sequence 6, Appl
44	792.5	17.3	839	2 US-08-457-880A-6	Sequence 6, Appl
45	792.5	17.3	839	3 US-08-444-622A-6	Sequence 6, Appl

## ALIGNMENTS

RESULT 1  
US-08-374-834-16  
Sequence 16, Application US/08374834

Patent No. 5656473

GENERAL INFORMATION:

APPLICANT: Valenzuela, et al.

TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Regeneron Pharmaceuticals, Inc.

STREET: 777 Old Saw Mill River Road

CITY: Tarrytown

STATE: New York

COUNTRY: USA

ZIP: 10591

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/374,834

FILING DATE: 19-JAN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/095,658

FILING DATE: 21-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Coberl, Robert J.

REGISTRATION NUMBER: 36,108

REFERENCE/DOCKET NUMBER: REG 190A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (914) 345-7400

TELEFAX: (914) 345-7721

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 869 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-374-834-16

Query Match 99.8%; Score 4558; DB 1; Length 869;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
DB 1 MRELVNIPVLHILTLVAFSGTEKLPKAPVITTTPTETVDALVEEYATMCAYESYPOEIS 60

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QY 61 WTRNKILIKLFDTRYISIRENGQLLTLLSVEDSDGICYCTANNVGAVGAVESGALOVKMK 120
DB 61 WTRNKILIKLFDTRYISIRENGQLLTLLSVEDSDGICYCTANNVGAVGAVESGALOVKMK 120
QY 121 PKITRPPINKKIIIEGKAVLPCTTMGNPKPSVMIGDPSLRNSRIAVLESGLRIHNV 180
DB 121 PKITRPPINKKIIIEGKAVLPCTTMGNPKPSVMIGDPSLRNSRIAVLESGLRIHNV 180
QY 181 OKEDAGYRCVANKSLGTAYSKVYKLEFEVFARILRAPESHNTFGSFVTLHCTATGIPV 240
DB 181 OKEDAGYRCVANKSLGTAYSKVYKLEFEVFARILRAPESHNTFGSFVTLHCTATGIPV 240
QY 241 PTTWIENGNAVSSGSIQESVKRVIDSRQLFTTRPGLTCTATNKHGKESTARAAT 300
DB 241 PTTWIENGNAVSSGSIQESVKRVIDSRQLFTTRPGLTCTATNKHGKESTARAAT 300
QY 301 ISTAEMSKPOKDNKGCAOYRGECNAVLAKDALVFLNTSYADPEEAOELLVHTANNEK 360
DB 301 ISTAEMSKPOKDNKGCAOYRGECNAVLAKDALVFLNTSYADPEEAOELLVHTANNEK 360
QY 361 VVSPVCRPAEALLCNHIFQECSPGVVPTPIPCREYCLAVALKELFCAKEMLVMEKTHRG 420
DB 361 VVSPVCRPAEALLCNHIFQECSPGVVPTPIPCREYCLAVALKELFCAKEMLVMEKTHRG 420
QY 421 LYSEMHLLSVPCSKLPSMHMDPTACARLPHLDYKNEKLTTPPMSSKPSVDIPLPS 480
DB 421 LYSEMHLLSVPCSKLPSMHMDPTACARLPHLDYKNEKLTTPPMSSKPSVDIPLPS 480
QY 481 SSSSFVSPTSMTVLIISMSFAIFVLLITTLVYCCRRRKQMKKKRESAAVTLTTL 540
DB 481 SSSSFVSPTSMTVLIISMSFAIFVLLITTLVYCCRRRKQMKKKRESAAVTLTTL 540
QY 541 SELLDRLHNPMTQORPMLLNPKLLSLEYPRNNIEYVRDIGGAFGRVQARAPGLLP 600
DB 541 SELLDRLHNPMTQORPMLLNPKLLSLEYPRNNIEYVRDIGGAFGRVQARAPGLLP 600
QY 601 EPTFMVAVKMLKEBASADMOADFOREALAEMFDPNIVKLGVCAAGKPMCLFEYMA 660
DB 601 EPTFMVAVKMLKEBASADMOADFOREALAEMFDPNIVKLGVCAAGKPMCLFEYMA 660
QY 661 GDLNEFLRSMSPHTVCSLSHSDLSMRQVSSPPPLSCAEOQLIARQVAAAGAYLSERK 720
DB 661 GDLNEFLRSMSPHTVCSLSHSDLSMRQVSSPPPLSCAEOQLIARQVAAAGAYLSERK 720
QY 721 FVHRDLATRCIYGENNVVVIADGSLRNITYSADYKANENDAIPIRMMPESIFRYRT 780
DB 721 FVHRDLATRCIYGENNVVVIADGSLRNITYSADYKANENDAIPIRMMPESIFRYRT 780
QY 781 TESDVMAVGVWLMEIFSYGLQPYYGMAHEEVIYVRDGNILSCPENCVELYNMLRLCWS 840
DB 781 TESDVMAVGVWLMEIFSYGLQPYYGMAHEEVIYVRDGNILSCPENCVELYNMLRLCWS 840
QY 841 KLPADRPSTSIHRIILRMCERAGTVSV 869
DB 841 KLPADRPSTSIHRIILRMCERAGTVSV 869

```

## RESULT 2

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US-08-644-271-29
Sequence 29, Application US/08644271
Patent No. 5814478
GENERAL INFORMATION:
APPLICANT: Valenzuela, et al.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS
TITLE OF INVENTION: AND LIGANDS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA

```

```

ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/644,271
FILING DATE: 10-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/008,657
FILING DATE: 15-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 195A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
TELEX:
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 869 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-644-271-29

Query Match 99.8%; Score 4558; DB 2; Length 869;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRELNVPIVHIITVAFSGTEKLPAPVITTELVDAIVEATFMCAVESYPOPEIS 60
DB 1 MRELNVPIVHIITVAFSGTEKLPAPVITTELVDAIVEATFMCAVESYPOPEIS 60
QY 61 WTRNKILIKLFDTRYISIRENGQLLTLLSVEDSDGICYCTANNVGAVGAVESGALOVKMK 120
DB 61 WTRNKILIKLFDTRYISIRENGQLLTLLSVEDSDGICYCTANNVGAVGAVESGALOVKMK 120
QY 121 PKITRPPINKKIIIEGKAVLPCTTMGNPKPSVMIGDPSLRNSRIAVLESGLRIHNV 180
DB 121 PKITRPPINKKIIIEGKAVLPCTTMGNPKPSVMIGDPSLRNSRIAVLESGLRIHNV 180
QY 181 OKEDAGYRCVANKSLGTAYSKVYKLEFEVFARILRAPESHNTFGSFVTLHCTATGIPV 240
DB 181 OKEDAGYRCVANKSLGTAYSKVYKLEFEVFARILRAPESHNTFGSFVTLHCTATGIPV 240
QY 241 PTTWIENGNAVSSGSIQESVKRVIDSRQLFTTRPGLTCTATNKHGKESTARAAT 300
DB 241 PTTWIENGNAVSSGSIQESVKRVIDSRQLFTTRPGLTCTATNKHGKESTARAAT 300
QY 301 ISTAEMSKPOKDNKGCAOYRGECNAVLAKDALVFLNTSYADPEEAOELLVHTANNEK 360
DB 301 ISTAEMSKPOKDNKGCAOYRGECNAVLAKDALVFLNTSYADPEEAOELLVHTANNEK 360
QY 361 VVSPVCRPAEALLCNHIFQECSPGVVPTPIPCREYCLAVALKELFCAKEMLVMEKTHRG 420
DB 361 VVSPVCRPAEALLCNHIFQECSPGVVPTPIPCREYCLAVALKELFCAKEMLVMEKTHRG 420
QY 421 LYSEMHLLSVPCSKLPSMHMDPTACARLPHLDYKNEKLTTPPMSSKPSVDIPLPS 480
DB 421 LYSEMHLLSVPCSKLPSMHMDPTACARLPHLDYKNEKLTTPPMSSKPSVDIPLPS 480
QY 481 SSSSFVSPTSMTVLIISMSFAIFVLLITTLVYCCRRRKQMKKKRESAAVTLTTL 540
DB 481 SSSSFVSPTSMTVLIISMSFAIFVLLITTLVYCCRRRKQMKKKRESAAVTLTTL 540
QY 541 SELLDRLHNPMTQORPMLLNPKLLSLEYPRNNIEYVRDIGGAFGRVQARAPGLLP 600
DB 541 SELLDRLHNPMTQORPMLLNPKLLSLEYPRNNIEYVRDIGGAFGRVQARAPGLLP 600

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QY 601 EPTMVAVKMLKEASADQADFORAALMAEFDPNPITVKLIGCAVCKPMLCFEYMA 660
DB 601 EPTMVAVKMLKEASADQADFORAALMAEFDPNPITVKLIGCAVCKPMLCFEYMA 660
QY 661 GDLNEFLRSMSPHTVCSLSHSDLSMRAOVSSPGPPPLSCAEOLCIAROVAAGMAYLSERK 720
DB 661 GDLNEFLRSMSPHTVCSLSHSDLSMRAOVSSPGPPPLSCAEOLCIAROVAAGMAYLSERK 720
QY 721 FVHRDLATRNCLVGENNVAVKIADFGLSRNTYSADYKANENDAIPIRMMPESIFNRYT 780
DB 721 FVHRDLATRNCLVGENNVAVKIADFGLSRNTYSADYKANENDAIPIRMMPESIFNRYT 780
QY 781 TESVMAVGYVLMWEIFSYGLQPYYGMAHEEVIYVRDGNILSCPENCPELYNIMRLCWS 840
DB 781 TESVMAVGYVLMWEIFSYGLQPYYGMAHEEVIYVRDGNILSCPENCPELYNIMRLCWS 840
QY 841 KLPADRPSTSIHRIILERMCEERAGETVS 869
DB 841 KLPADRPSTSIHRIILERMCEERAGETVS 869

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RESULT 3
US-09-077-955-33
; Sequence 33, Application US/09077955A
; Patent No. 6413740
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al., David M.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
; FILE REFERENCE: REG195-B-PCR-US
; CURRENT APPLICATION NUMBER: US/09/077, 955A
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: PCT/US96/20696
; EARLIER FILING DATE: 1996-12-13
; EARLIER APPLICATION NUMBER: 08/644, 271
; EARLIER FILING DATE: 1996-05-10
; EARLIER APPLICATION NUMBER: 60/008,657
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 869
; TYPE: PRT
; ORGANISM: Homo sapiens
S-09-077-955-33

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Query Match 99.8%; Score 4558; DB 4; Length 869;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MELVNIPIVHLITLVAFGSTKLPKAPVITTPLETVDAVVEVATFMCVAVESYPOPEIS 60
DB 1 MELVNIPIVHLITLVAFGSTKLPKAPVITTPLETVDAVVEVATFMCVAVESYPOPEIS 60
QY 61 WTRNKLILKLFDTKRSIRENGQLTILSVESDDGIYCTTANGVGVAVESGALOVKKK 120
DB 61 WTRNKLILKLFDTKRSIRENGQLTILSVESDDGIYCTTANGVGVAVESGALOVKKK 120
QY 121 PRTTTPPIVVKTIIEGLKATLPCTTMGNRPVSWIKGDSPLRENSRIAVLESGLRIHNV 180
DB 121 PRTTTPPIVVKTIIEGLKATLPCTTMGNRPVSWIKGDSPLRENSRIAVLESGLRIHNV 180
QY 181 OKEDAGORYCAVAKNSLGTAYSKVVKLEFEVFARILRAPSHVTFGSPFTLHCTATGTPV 240
DB 181 OKEDAGORYCAVAKNSLGTAYSKVVKLEFEVFARILRAPSHVTFGSPFTLHCTATGTPV 240
QY 241 PRTTTPPIVVKTIIEGLKATLPCTTMGNRPVSWIKGDSPLRENSRIAVLESGLRIHNV 300
DB 241 PRTTTPPIVVKTIIEGLKATLPCTTMGNRPVSWIKGDSPLRENSRIAVLESGLRIHNV 300
QY 301 ISIAEMSRPKDNKGYCAQYRGECVNAVIAKDALVFLMTSTADPEADELLVHTAMNEIK 360
DB 301 ISIAEMSRPKDNKGYCAQYRGECVNAVIAKDALVFLMTSTADPEADELLVHTAMNEIK 360

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QY 361 VVSFVCRPAEALLCNHIFQECSPGVPTPIPICREYCLAVKELFCAKEMWMEKTHRG 420
DB 361 VVSFVCRPAEALLCNHIFQECSPGVPTPIPICREYCLAVKELFCAKEMWMEKTHRG 420
QY 421 LYREEMHLLSVKCSKLPMSHMDPTACARLPHLDYKNEENLKTFFPMTSSKPSVDIPULPS 480
DB 421 LYREEMHLLSVKCSKLPMSHMDPTACARLPHLDYKNEENLKTFFPMTSSKPSVDIPULPS 480
QY 481 SSSSFVSPTYSMTVITISIMSFAIFVLLITTLTYCCRRRKQKKNKRESAAVTLTTL 540
DB 481 SSSSFVSPTYSMTVITISIMSFAIFVLLITTLTYCCRRRKQKKNKRESAAVTLTTL 540
QY 541 SELLDLHNPMPYQRPPLINPKLSLEYPRNNIEYVRDIEGAGFVQARAPGLLPY 600
DB 541 SELLDLHNPMPYQRPPLINPKLSLEYPRNNIEYVRDIEGAGFVQARAPGLLPY 600
QY 601 EPTMVAVKMLKEASADQADFORAALMAEFDPNPITVKLIGCAVCKPMLCFEYMA 660
DB 601 EPTMVAVKMLKEASADQADFORAALMAEFDPNPITVKLIGCAVCKPMLCFEYMA 660
QY 661 GDLNEFLRSMSPHTVCSLSHSDLSMRAOVSSPGPPPLSCAEOLCIAROVAAGMAYLSERK 720
DB 661 GDLNEFLRSMSPHTVCSLSHSDLSMRAOVSSPGPPPLSCAEOLCIAROVAAGMAYLSERK 720
QY 721 FVHRDLATRNCLVGENNVAVKIADFGLSRNTYSADYKANENDAIPIRMMPESIFNRYT 780
DB 721 FVHRDLATRNCLVGENNVAVKIADFGLSRNTYSADYKANENDAIPIRMMPESIFNRYT 780
QY 781 TESVMAVGYVLMWEIFSYGLQPYYGMAHEEVIYVRDGNILSCPENCPELYNIMRLCWS 840
DB 781 TESVMAVGYVLMWEIFSYGLQPYYGMAHEEVIYVRDGNILSCPENCPELYNIMRLCWS 840
QY 841 KLPADRPSTSIHRIILERMCEERAGETVS 869
DB 841 KLPADRPSTSIHRIILERMCEERAGETVS 869

```

```

RESULT 4
US-08-374-834-1
; Sequence 1, Application US/08374834
; Patent No. 5636473
; GENERAL INFORMATION:
; APPLICANT: Valenzuela, et al.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/374,834
; FILING DATE: 19-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/095,658
; FILING DATE: 21-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Covert, Robert J.
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 190A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-7721
; INFORMATION FOR SEQ ID NO: 1:

```

SEQUENCE CHARACTERISTICS:  
 LENGTH: 868 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 US-08-374-834-1

Query Match 93.9%; Score 4292.5; DB 1; Length 868;  
 Best Local Similarity 93.2%; Pred. No. 0;  
 Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

QY 1 MRLVNIPLVHLITLVAASGTEKLPKAPVITPTLETVDAIVEVATFMCVAVESYPOPEIS 60  
 DB 1 MRLVNIPLVHLITLVAASGTEKLPKAPVITPTLETVDAIVEVATFMCVAVESYPOPEIS 60  
 QY 61 WTRNKILIKLFDTRYISIRENGQLTLISVEDSDGIYCTANNNGVAVESGALQVKKK 120  
 DB 61 WTRNKILIKLFDTRYISIRENGQLTLISVEDSDGIYCTANNNGVAVESGALQVKKK 120  
 QY 121 PKITRPPINVKIIEGLKAVLPCTTMGNPKPSVWIKGDSPLRNSRIAVLESGLRIHNV 180  
 DB 121 PKITRPPINVKIIEGLKAVLPCTTMGNPKPSVWIKGDSPLRNSRIAVLESGLRIHNV 180  
 QY 181 OKEDAGQRCVAKNSIGTAVSKVVKLEFEVFAIRILAPESHNTFSGSVTLHCTATGIPV 240  
 DB 181 OKEDAGQRCVAKNSIGTAVSKVVKLEFEVFAIRILAPESHNTFSGSVTLHCTATGIPV 240  
 QY 241 PTTIWIENGNAVSSGSIQESVKDVIDSRQLQLEITPKGLYTCTATNKHGKSTAKAAAT 300  
 DB 241 PTTIWIENGNAVSSGSIQESVKDVIDSRQLQLEITPKGLYTCTATNKHGKSTAKAAAT 300  
 QY 301 ISTAEMSKPOKDNKGCAQYRGVCNVAVLAKDALVPLNTSYADPEEAQELLVHTANNEIK 360  
 DB 301 ISTAEMSKPOKDNKGCAQYRGVCNVAVLAKDALVPLNTSYADPEEAQELLVHTANNEIK 360  
 QY 360 VSTIAEMSKQESKGCACQYRGVCNVAVLAKDALVPLNTSYADPEEAQELLVHTANNEIK 360  
 DB 360 VSTIAEMSKQESKGCACQYRGVCNVAVLAKDALVPLNTSYADPEEAQELLVHTANNEIK 360  
 QY 420 VVSPVCPAPAEALLCNHIFQECSPGVVPTPIICREYCLAVKELFCAKELVMEERTHNG 420  
 DB 420 VVSPVCPAPAEALLCNHIFQECSPGVVPTPIICREYCLAVKELFCAKELVMEERTHNG 420  
 QY 420 AVSPDLCPAPAEALLCNHIFQECSPGVVPTPIICREYCLAVKELFCAKELVMEERTHNG 420  
 DB 420 AVSPDLCPAPAEALLCNHIFQECSPGVVPTPIICREYCLAVKELFCAKELVMEERTHNG 420  
 QY 480 LYSEMHLSVPCSKSLPSHMDPTACARLPHLDYKKNELKTPPTSSPSVDINLP 480  
 DB 480 LYSEMHLSVPCSKSLPSHMDPTACARLPHLDYKKNELKTPPTSSPSVDINLP 480  
 QY 480 LYSGMHFLFVPCSKSLPSHMDPTACARLPHLDYKKNELKTPPTSSPSVDINLP 480  
 DB 480 LYSGMHFLFVPCSKSLPSHMDPTACARLPHLDYKKNELKTPPTSSPSVDINLP 480  
 QY 540 SSSSFSVSPYEMTVIISMSFAIFVLLITLTYCCRRRKKMKKRESAAVTLTTLTP 540  
 DB 540 SSSSFSVSPYEMTVIISMSFAIFVLLITLTYCCRRRKKMKKRESAAVTLTTLTP 540  
 QY 540 SELLDRLHPNMYQRPMLLNPKLSLEYPRNNIEYVDIGSAGRGVQAAPGLLP 600  
 DB 540 SELLDRLHPNMYQRPMLLNPKLSLEYPRNNIEYVDIGSAGRGVQAAPGLLP 600  
 QY 600 EPTTMAVAVKMKKEASADMDADFORAALMAEFDPNPIYKLVGCAVAGKMCLEFEMAY 660  
 DB 600 EPTTMAVAVKMKKEASADMDADFORAALMAEFDPNPIYKLVGCAVAGKMCLEFEMAY 660  
 QY 660 GDLNEFLRSMSPHTVCLSHSDLSSTRARVSSPGPPPLSCAEQCLIAQVAAAGMAYLSERK 719  
 DB 660 GDLNEFLRSMSPHTVCLSHSDLSSTRARVSSPGPPPLSCAEQCLIAQVAAAGMAYLSERK 719  
 QY 721 FVHDLATRNCLVGENNVKIADEGLSRNIYSADYIYANENDALPIRMMPESTFYRYT 780  
 DB 721 FVHDLATRNCLVGENNVKIADEGLSRNIYSADYIYANENDALPIRMMPESTFYRYT 780  
 QY 781 TESVMAVGVVIMFISYGLQPYGMAHEEVIYVRGNILSCPENGVETLYNLMRCMS 840  
 DB 781 TESVMAVGVVIMFISYGLQPYGMAHEEVIYVRGNILSCPENGVETLYNLMRCMS 840  
 QY 841 KLPADRSFTSIRILERMCEERAGTVSV 869  
 DB 840 KLPADRSFTSIRILERMCEERAGTVSV 868

## RESULT 5

US-08-644-271-1

Sequence 1, Application US/08644271

Patent No. 5814478

GENERAL INFORMATION:

APPLICANT: Valenzuela, et al.

TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS

TITLE OF INVENTION: AND LIGANDS

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Regeneron Pharmaceuticals, Inc.

STREET: 777 Old Saw Mill Road

CITY: Tarrytown

STATE: NY

COUNTRY: USA

ZIP: 10591

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/644,271

FILING DATE: 10-MAY-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 60/008,657

FILING DATE: 15-DEC-1995

ATTORNEY/AGENT INFORMATION:

NAME: Codette, Robert J

REGISTRATION NUMBER: 36,108

REFERENCE/DOCKET NUMBER: REG 195A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 914-345-7400

TELEFAX: 914-345-7721

TELEX:

INFORMATION FOR SEQ. ID NO. 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 868 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-644-271-1

Query Match 93.9%; Score 4292.5; DB 2; Length 868;

Best Local Similarity 93.2%; Pred. No. 0;

Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

QY 1 MRLVNIPLVHLITLVAASGTEKLPKAPVITPTLETVDAIVEVATFMCVAVESYPOPEIS 60  
 DB 1 MRLVNIPLVHLITLVAASGTEKLPKAPVITPTLETVDAIVEVATFMCVAVESYPOPEIS 60  
 QY 61 WTRNKILIKLFDTRYISIRENGQLTLISVEDSDGIYCTANNNGVAVESGALQVKKK 120  
 DB 61 WTRNKILIKLFDTRYISIRENGQLTLISVEDSDGIYCTANNNGVAVESGALQVKKK 120  
 QY 121 PKITRPPINVKIIEGLKAVLPCTTMGNPKPSVWIKGDSPLRNSRIAVLESGLRIHNV 180  
 DB 121 PKITRPPINVKIIEGLKAVLPCTTMGNPKPSVWIKGDSPLRNSRIAVLESGLRIHNV 180  
 QY 181 OKEDAGQRCVAKNSIGTAVSKVVKLEFEVFAIRILAPESHNTFSGSVTLHCTATGIPV 240  
 DB 181 OKEDAGQRCVAKNSIGTAVSKVVKLEFEVFAIRILAPESHNTFSGSVTLHCTATGIPV 240  
 QY 241 PTTIWIENGNAVSSGSIQESVKDVIDSRQLQLEITPKGLYTCTATNKHGKSTAKAAAT 300  
 DB 241 PTTIWIENGNAVSSGSIQESVKDVIDSRQLQLEITPKGLYTCTATNKHGKSTAKAAAT 300  
 QY 301 ISTAEMSKPOKDNKGCAQYRGVCNVAVLAKDALVPLNTSYADPEEAQELLVHTANNEIK 360  
 DB 301 ISTAEMSKPOKDNKGCAQYRGVCNVAVLAKDALVPLNTSYADPEEAQELLVHTANNEIK 360



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QY 361 VSPVCRPAEALLCNHIFQECSPGVPTPIPICREYCLAVKEIFCAKEMLVMEKTHRG 420
DB 361 AVSPICRPAEALLCNHIFQECSPGVPTPIPICREYCLAVKEIFCAKEMLVMEKTHRG 420
QY 421 LYRSMHLLSVKPKCSKLPMSHMDPTACARLPHLDYKNENKLTFFPMTSKSPVDIPNLP 480
DB 421 LYRSMHLLSVKPKCSKLPMSHMDPTACARLPHLDYKNENKLTFFPMTSKSPVDIPNLP 480
QY 481 SSSSFVSPTYSMTVTIISMSFAIFVLTITTLCCRRRKKKKRESAAVTLTLP 540
DB 480 ASTSPFASVAMTIVTISMSFAIFVLTITTLCCRRRKKKKRESAAVTLTLP 539
QY 541 SELLDRLHNPMTQRPMLNPKLSTLEYRNNIEYVRDIGEAGFGRVQARAPGLLP 600
DB 540 SELLDRLHNPMTQRPMLNPKLSTLEYRNNIEYVRDIGEAGFGRVQARAPGLLP 599
QY 601 EPTFMVAVKMKKEASADMDQADFORAALMAEFDNPNTVLLGVCAVGRPMCLTFEYMA 660
DB 600 EPTFMVAVKMKKEASADMDQADFORAALMAEFDNPNTVLLGVCAVGRPMCLTFEYMA 659
QY 661 GDLNEFLRSMSPHTVCSLSHSDLSMRAOVSSPPGPLSCAEQICIAQVAAAGAYLSERK 720
DB 660 GDLNEFLRSMSPHTVCSLSHSDLSMRAOVSSPPGPLSCAEQICIAQVAAAGAYLSERK 719
QY 721 FVHRDLATNCLVGENNVKIAIDFGLSRNTYSADYKANKENDAIPIRMMPESIFYRNT 780
DB 720 FVHRDLATNCLVGENNVKIAIDFGLSRNTYSADYKANKENDAIPIRMMPESIFYRNT 779
QY 781 TESDVAVGVVLMETFSYGLQPYGYMAHEVITYVRDGNILSCPENCPVELYNMLRLCWS 840
DB 780 TESDVAVGVVLMETFSYGLQPYGYMAHEVITYVRDGNILSCPENCPVELYNMLRLCWS 839
QY 841 KLPADRPSTSTHRIILERCERAEGETVSV 869
DB 840 KLPADRPSTSTHRIILERCERAEGETVSV 868

RESULT 6
US-09-077-955-1
; Sequence 1, Application US/09077955A
; Patent No. 6413740
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al., David M.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
; FILE REFERENCE: REG195-B-PCT-US
; CURRENT APPLICATION NUMBER: US/09/077,955A
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: PCT/US96/20696
; EARLIER FILING DATE: 1996-12-13
; EARLIER APPLICATION NUMBER: 08/644,271
; EARLIER FILING DATE: 1996-05-10
; EARLIER APPLICATION NUMBER: 60/008,657
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 868
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-077-955-1

Query Match 93.9%; Score 4292.5; DB 4; Length 868;
Best Local Similarity 93.2%; Pred. No. 0;
Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

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QY 121 PKTRPPIVVKIIIEGLKAVLDPCTTMGNKPSVSWIKGDSPLRENSRIAVLESGSLRIHNV 180
DB 121 PKTRPPIVVKIIIEGLKAVLDPCTTMGNKPSVSWIKGDSPLRENSRIAVLESGSLRIHNV 180
QY 181 OKEDAGORCAVAKNSLSGAYSKVYKLEEVARILIRAPESHNVTFGSFVTLHCTATGIPV 240
DB 181 OKEDAGORCAVAKNSLSGAYSKVYKLEEVARILIRAPESHNVTFGSFVTLHCTATGIPV 240
QY 241 PTIWIENGNAVSSGSIQESVYKDVIRSLQFLTFTKGLYCIATNNHGEFSTAKAAAT 300
DB 241 PTIWIENGNAVSSGSIQESVYKDVIRSLQFLTFTKGLYCIATNNHGEFSTAKAAAT 300
QY 301 ISTAEKSPQDKNGCYCAQYRGEVCNAVLAKDALVFNLTNSYADPEAOELLVHTANMELK 360
DB 301 ISTAEKSPQDKNGCYCAQYRGEVCNAVLAKDALVFNLTNSYADPEAOELLVHTANMELK 360
QY 361 VSPVCRPAEALLCNHIFQECSPGVPTPIPICREYCLAVKEIFCAKEMLVMEKTHRG 420
DB 361 AVSPICRPAEALLCNHIFQECSPGVPTPIPICREYCLAVKEIFCAKEMLVMEKTHRG 420
QY 421 LYRSMHLLSVKPKCSKLPMSHMDPTACARLPHLDYKNENKLTFFPMTSKSPVDIPNLP 480
DB 421 LYRSMHLLSVKPKCSKLPMSHMDPTACARLPHLDYKNENKLTFFPMTSKSPVDIPNLP 479
QY 481 SSSSFVSPTYSMTVTIISMSFAIFVLTITTLCCRRRKKKKRESAAVTLTLP 540
DB 480 ASTSPFASVAMTIVTISMSFAIFVLTITTLCCRRRKKKKRESAAVTLTLP 539
QY 541 SELLDRLHNPMTQRPMLNPKLSTLEYRNNIEYVRDIGEAGFGRVQARAPGLLP 600
DB 540 SELLDRLHNPMTQRPMLNPKLSTLEYRNNIEYVRDIGEAGFGRVQARAPGLLP 599
QY 601 EPTFMVAVKMKKEASADMDQADFORAALMAEFDNPNTVLLGVCAVGRPMCLTFEYMA 660
DB 600 EPTFMVAVKMKKEASADMDQADFORAALMAEFDNPNTVLLGVCAVGRPMCLTFEYMA 659
QY 661 GDLNEFLRSMSPHTVCSLSHSDLSMRAOVSSPPGPLSCAEQICIAQVAAAGAYLSERK 720
DB 660 GDLNEFLRSMSPHTVCSLSHSDLSMRAOVSSPPGPLSCAEQICIAQVAAAGAYLSERK 719
QY 721 FVHRDLATNCLVGENNVKIAIDFGLSRNTYSADYKANKENDAIPIRMMPESIFYRNT 780
DB 720 FVHRDLATNCLVGENNVKIAIDFGLSRNTYSADYKANKENDAIPIRMMPESIFYRNT 779
QY 781 TESDVAVGVVLMETFSYGLQPYGYMAHEVITYVRDGNILSCPENCPVELYNMLRLCWS 840
DB 780 TESDVAVGVVLMETFSYGLQPYGYMAHEVITYVRDGNILSCPENCPVELYNMLRLCWS 839
QY 841 KLPADRPSTSTHRIILERCERAEGETVSV 869
DB 840 KLPADRPSTSTHRIILERCERAEGETVSV 868

RESULT 7
PCT-US95-08493-21
; Sequence 21, Application PC/TUS9508493
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive
; APPLICANT: Caruso, Anthony
; TITLE OF INVENTION: Novel mlk Receptor Tyrosine Kinases
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEGAL AFFAIRS
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/08493  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brown, Scott A  
 REGISTRATION NUMBER: 32,724  
 REFERENCE/DOCKET NUMBER: G15234A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 498-8224  
 TELEFAX: (617) 876-5851  
 INFORMATION FOR SEQ ID NO: 21:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 868 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US95-08493-21

Query Match 93.4%; Score 4269.5; DB 5; Length 868;  
 Best Local Similarity 92.9%; Pred. No. 0;  
 Matches 807; Conservative 30; Mismatches 31; Indels 1; Gaps 1;

1 MRELVINPILVHILTLVAFSGTEKLPKAVITTTLETVDALVEVATFMCAYESYQPEIS 60  
 1 MRELVINPILVHILTLVAFSGTEKLPKAVITTTLETVDALVEVATFMCAYESYQPEIS 60  
 61 WTRNKILIKLFDTRYSIRENGQLLTLSVEDSDGIYCCCTANNVGGAVESGALQVKK 120  
 61 WTRNKILIKLFDTRYSIRENGQLLTLSVEDSDGIYCCCTANNVGGAVESGALQVKK 120  
 121 PKTRPPINVKIIIEGLKAVLPCTTMGNPKPSYSWIKGDSPLRENSRIAVLESGSLRIHV 180  
 121 PKTRPPINVKIIIEGLKAVLPCTTMGNPKPSYSWIKGDSPLRENSRIAVLESGSLRIHV 180  
 121 PKTRPPINVKIIIEGLKAVLPCTTMGNPKPSYSWIKGDSPLRENSRIAVLESGSLRIHV 180  
 181 QKEDAGQRCVANKSLGTAVSKVLEFEVFARILRAPSHNVTFGSFVTLHCTATGIV 240  
 181 QKEDAGQRCVANKSLGTAVSKVLEFEVFARILRAPSHNVTFGSFVTLHCTATGIV 240  
 181 QKEDAGQRCVANKSLGTAVSKVLEFEVFARILRAPSHNVTFGSFVTLHCTATGIV 240  
 241 PTTWINGNAVSSGSIQESVDRVIDSLQLFTKPGLYTCTIATNKHGKSTAKAAAT 300  
 241 PTTWINGNAVSSGSIQESVDRVIDSLQLFTKPGLYTCTIATNKHGKSTAKAAAT 300  
 241 PTTWINGNAVSSGSIQESVDRVIDSLQLFTKPGLYTCTIATNKHGKSTAKAAAT 300  
 301 ISIAEMSKPOKNGKCAQYRGVCAVLAADALVPLNTSYADPEAOELVHTANNEK 360  
 301 ISIAEMSKPOKNGKCAQYRGVCAVLAADALVPLNTSYADPEAOELVHTANNEK 360  
 301 VSTIAEMSKPOKNGKCAQYRGVCAVLAADALVPLNTSYADPEAOELVHTANNEK 360  
 361 VSPVCPRAAEALLCNHIFQECSPGVVPTPIPCREYCLAVKELFCAKEMLVMEKTHRG 420  
 361 VSPVCPRAAEALLCNHIFQECSPGVVPTPIPCREYCLAVKELFCAKEMLVMEKTHRG 420  
 361 VSPVCPRAAEALLCNHIFQECSPGVVPTPIPCREYCLAVKELFCAKEMLVMEKTHRG 420  
 421 LYRSEMHLLSVPCSKSLPSMHPDPTACALPHLDYKKNLKEPMTSSKPSVDINPLS 480  
 421 LYRSEMHLLSVPCSKSLPSMHPDPTACALPHLDYKKNLKEPMTSSKPSVDINPLS 480  
 421 LYRSEMHLLSVPCSKSLPSMHPDPTACALPHLDYKKNLKEPMTSSKPSVDINPLS 480  
 481 SSSSSSVSPTEYMTYIISMSFAIFVLLITTLTYCCRRRQKMKKRESAAVLTTLTP 540  
 481 SSSSSSVSPTEYMTYIISMSFAIFVLLITTLTYCCRRRQKMKKRESAAVLTTLTP 540  
 481 SSSSSSVSPTEYMTYIISMSFAIFVLLITTLTYCCRRRQKMKKRESAAVLTTLTP 540  
 480 ASISSVSPAYEMTYIISVSSFAIFVLLITTLTYCCRRRQKMKKRESAAVLTTLTP 539  
 480 ASISSVSPAYEMTYIISVSSFAIFVLLITTLTYCCRRRQKMKKRESAAVLTTLTP 539  
 480 ASISSVSPAYEMTYIISVSSFAIFVLLITTLTYCCRRRQKMKKRESAAVLTTLTP 539  
 541 SELLDRLHPNMYQRMPLLNKRLSLETPRNNEIEVRDYGAGRGVQAARAPGLPY 600  
 541 SELLDRLHPNMYQRMPLLNKRLSLETPRNNEIEVRDYGAGRGVQAARAPGLPY 600  
 541 SELLDRLHPNMYQRMPLLNKRLSLETPRNNEIEVRDYGAGRGVQAARAPGLPY 600  
 540 SELLDRLHPNMYQRMPLLNKRLSLETPRNNEIEVRDYGAGRGVQAARAPGLPY 599  
 540 SELLDRLHPNMYQRMPLLNKRLSLETPRNNEIEVRDYGAGRGVQAARAPGLPY 599  
 540 SELLDRLHPNMYQRMPLLNKRLSLETPRNNEIEVRDYGAGRGVQAARAPGLPY 599  
 601 EPTTMAVVKMLKEBASADMOADQREAAALAEFDNPNIVKLLGCAVAGKPMCLFEYMA 660  
 601 EPTTMAVVKMLKEBASADMOADQREAAALAEFDNPNIVKLLGCAVAGKPMCLFEYMA 660  
 601 EPTTMAVVKMLKEBASADMOADQREAAALAEFDNPNIVKLLGCAVAGKPMCLFEYMA 660  
 600 EPTTMAVVKMLKEBASADMOADQREAAALAEFDNPNIVKLLGCAVAGKPMCLFEYMA 659  
 600 EPTTMAVVKMLKEBASADMOADQREAAALAEFDNPNIVKLLGCAVAGKPMCLFEYMA 659  
 600 EPTTMAVVKMLKEBASADMOADQREAAALAEFDNPNIVKLLGCAVAGKPMCLFEYMA 659  
 661 GDINEFLRSMSPHTVCSLSHSDLSMRAOVSSPGPPPLSCABOCLIAQVAAAGAYLSERK 720  
 661 GDINEFLRSMSPHTVCSLSHSDLSMRAOVSSPGPPPLSCABOCLIAQVAAAGAYLSERK 720  
 661 GDINEFLRSMSPHTVCSLSHSDLSMRAOVSSPGPPPLSCABOCLIAQVAAAGAYLSERK 720  
 660 GDINEFLRSMSPHTVCSLSHSDLSMRAOVSSPGPPPLSCABOCLIAQVAAAGAYLSERK 719  
 660 GDINEFLRSMSPHTVCSLSHSDLSMRAOVSSPGPPPLSCABOCLIAQVAAAGAYLSERK 719  
 660 GDINEFLRSMSPHTVCSLSHSDLSMRAOVSSPGPPPLSCABOCLIAQVAAAGAYLSERK 719  
 721 FVHRDLATRNCLVGENNVVRIADGSLRNITYSADYANENNDALPIRMMPESIFYNRYT 780  
 721 FVHRDLATRNCLVGENNVVRIADGSLRNITYSADYANENNDALPIRMMPESIFYNRYT 780  
 721 FVHRDLATRNCLVGENNVVRIADGSLRNITYSADYANENNDALPIRMMPESIFYNRYT 780

720 FVHRDLATRNCLVGENNVVRIADGSLRNITYSADYANENNDALPIRMMPESIFYNRYT 779  
 781 TESDVNAVGVVLEWIEISYGLQPYGMAHEEVIYVDRGNILSPENCPELILMLCLMS 840  
 781 TESDVNAVGVVLEWIEISYGLQPYGMAHEEVIYVDRGNILSPENCPELILMLCLMS 840  
 780 TESDVNAVGVVLEWIEISYGLQPYGMAHEEVIYVDRGNILSPENCPELILMLCLMS 839  
 841 KLPADRSFSTIRILERMCEBAGTYSV 869  
 841 KLPADRSFSTIRILERMCEBAGTYSV 869  
 840 KLPADRSFSTIRILERMCEBAGTYSV 868

RESULT 8  
 PCT-US95-08493-19  
 Sequence 19, Application PC/TUS9508493

GENERAL INFORMATION:  
 APPLICANT: Wood, Clive  
 APPLICANT: Caruso, Anthony  
 TITLE OF INVENTION: Novel mlk Receptor Tyrosine Kinases  
 NUMBER OF SEQUENCES: 21  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LEGAL AFFAIRS  
 STREET: 87 Cambridgepark Drive  
 CITY: Cambridge  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02140

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/08493  
 FILING DATE:

CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brown, Scott A  
 REGISTRATION NUMBER: 32,724  
 REFERENCE/DOCKET NUMBER: G15234A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 498-8224  
 TELEFAX: (617) 876-5851  
 INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 860 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US95-08493-19

Query Match 92.4%; Score 4220.5; DB 5; Length 860;  
 Best Local Similarity 92.2%; Pred. No. 0;  
 Matches 801; Conservative 29; Mismatches 30; Indels 9; Gaps 2;

1 MRELVINPILVHILTLVAFSGTEKLPKAVITTTLETVDALVEVATFMCAYESYQPEIS 60  
 1 MRELVINPILVHILTLVAFSGTEKLPKAVITTTLETVDALVEVATFMCAYESYQPEIS 60  
 61 WTRNKILIKLFDTRYSIRENGQLLTLSVEDSDGIYCCCTANNVGGAVESGALQVKK 120  
 61 WTRNKILIKLFDTRYSIRENGQLLTLSVEDSDGIYCCCTANNVGGAVESGALQVKK 120  
 121 PKTRPPINVKIIIEGLKAVLPCTTMGNPKPSYSWIKGDSPLRENSRIAVLESGSLRIHV 180  
 121 PKTRPPINVKIIIEGLKAVLPCTTMGNPKPSYSWIKGDSPLRENSRIAVLESGSLRIHV 180  
 121 PKTRPPINVKIIIEGLKAVLPCTTMGNPKPSYSWIKGDSPLRENSRIAVLESGSLRIHV 180  
 181 QKEDAGQRCVANKSLGTAVSKVLEFEVFARILRAPSHNVTFGSFVTLHCTATGIV 240  
 181 QKEDAGQRCVANKSLGTAVSKVLEFEVFARILRAPSHNVTFGSFVTLHCTATGIV 240  
 181 QKEDAGQRCVANKSLGTAVSKVLEFEVFARILRAPSHNVTFGSFVTLHCTATGIV 240  
 241 PTTWINGNAVSSGSIQESVDRVIDSLQLFTKPGLYTCTIATNKHGKSTAKAAAT 300  
 241 PTTWINGNAVSSGSIQESVDRVIDSLQLFTKPGLYTCTIATNKHGKSTAKAAAT 300  
 241 PTTWINGNAVSSGSIQESVDRVIDSLQLFTKPGLYTCTIATNKHGKSTAKAAAT 300  
 301 ISIAEMSKPOKNGKCAQYRGVCAVLAADALVPLNTSYADPEAOELVHTANNEK 360  
 301 ISIAEMSKPOKNGKCAQYRGVCAVLAADALVPLNTSYADPEAOELVHTANNEK 360  
 301 VSTIAEMSKPOKNGKCAQYRGVCAVLAADALVPLNTSYADPEAOELVHTANNEK 360  
 361 VSPVCPRAAEALLCNHIFQECSPGVVPTPIPCREYCLAVKELFCAKEMLVMEKTHRG 420  
 361 VSPVCPRAAEALLCNHIFQECSPGVVPTPIPCREYCLAVKELFCAKEMLVMEKTHRG 420  
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 421 LYRSEMHLLSVPCSKSLPSMHPDPTACALPHLDYKKNLKEPMTSSKPSVDINPLS 480  
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 481 SSSSSSVSPTEYMTYIISMSFAIFVLLITTLTYCCRRRQKMKKRESAAVLTTLTP 540  
 481 SSSSSSVSPTEYMTYIISMSFAIFVLLITTLTYCCRRRQKMKKRESAAVLTTLTP 540  
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 541 SELLDRLHPNMYQRMPLLNKRLSLETPRNNEIEVRDYGAGRGVQAARAPGLPY 600  
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 540 SELLDRLHPNMYQRMPLLNKRLSLETPRNNEIEVRDYGAGRGVQAARAPGLPY 599  
 601 EPTTMAVVKMLKEBASADMOADQREAAALAEFDNPNIVKLLGCAVAGKPMCLFEYMA 660  
 601 EPTTMAVVKMLKEBASADMOADQREAAALAEFDNPNIVKLLGCAVAGKPMCLFEYMA 660  
 601 EPTTMAVVKMLKEBASADMOADQREAAALAEFDNPNIVKLLGCAVAGKPMCLFEYMA 660  
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 600 EPTTMAVVKMLKEBASADMOADQREAAALAEFDNPNIVKLLGCAVAGKPMCLFEYMA 659  
 661 GDINEFLRSMSPHTVCSLSHSDLSMRAOVSSPGPPPLSCABOCLIAQVAAAGAYLSERK 720  
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 661 GDINEFLRSMSPHTVCSLSHSDLSMRAOVSSPGPPPLSCABOCLIAQVAAAGAYLSERK 720  
 660 GDINEFLRSMSPHTVCSLSHSDLSMRAOVSSPGPPPLSCABOCLIAQVAAAGAYLSERK 719  
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 660 GDINEFLRSMSPHTVCSLSHSDLSMRAOVSSPGPPPLSCABOCLIAQVAAAGAYLSERK 719  
 721 FVHRDLATRNCLVGENNVVRIADGSLRNITYSADYANENNDALPIRMMPESIFYNRYT 780  
 721 FVHRDLATRNCLVGENNVVRIADGSLRNITYSADYANENNDALPIRMMPESIFYNRYT 780  
 721 FVHRDLATRNCLVGENNVVRIADGSLRNITYSADYANENNDALPIRMMPESIFYNRYT 780

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QY 301 ISAEWSKPKQDNKGYCAQYRGEVCNAYLAKDALVFLNTSYADPEAEQELLVHTANNEK 360
DB 301 VSIEMSKSQKDSQGYCAQYRGEVCNAYLAKDALVFLNTSYADPEAEQELLVHTANNEK 360
QY 361 VVSVCRAAALACNHIPOECSPGVVPTPIPIREXCLAVKELEFCAKEMLVMEKTHRG 420
DB 361 AVSPLCRPAEALACNHIPOECSPGVVPTPIPIREXCLAVKELEFCAKEMLVMEKTHRG 420
QY 421 LYRESEHMLSVKCSKIPSMHMDPTACARLPHLDYNNENKLTFFPMNISKSVIPNIPS 480
DB 421 LYRSGHMLLPVPECSKIPSMHMDPTACARLPHLDYNNENKLTFFPMNISKSVIPNIPS 480
QY 481 SSSSESVSPYMTVITISMSFAIFVLLITLTYCCRRRQKMKKKRESAAVTLTTLTP 540
DB 481 SSSSESVSPYMTVITISMSFAIFVLLITLTYCCRRRQKMKKKRESAAVTLTTLTP 540
QY 472 ASTSSFAVSPAYMTVITISMSFAIFVLLITLTYCCRRRQKMKKKRESAAVTLTTLTP 531
DB 472 ASTSSFAVSPAYMTVITISMSFAIFVLLITLTYCCRRRQKMKKKRESAAVTLTTLTP 531
QY 541 SELLDRLHPNPMYORPRLNPKLLNPKLLNPKLLNPKLLNPKLLNPKLLNPKLLNPKLLN 600
DB 541 SELLDRLHPNPMYORPRLNPKLLNPKLLNPKLLNPKLLNPKLLNPKLLNPKLLNPKLLN 600
QY 532 SELLDRLHPNPMYORPRLNPKLLNPKLLNPKLLNPKLLNPKLLNPKLLNPKLLNPKLLN 591
DB 532 SELLDRLHPNPMYORPRLNPKLLNPKLLNPKLLNPKLLNPKLLNPKLLNPKLLNPKLLN 591
QY 601 EPTMVAVKMLKEASADMOADPQREALALAEFDNPIVLLGVCAGKPMCLLEFEMAY 660
DB 601 EPTMVAVKMLKEASADMOADPQREALALAEFDNPIVLLGVCAGKPMCLLEFEMAY 660
QY 592 EPTMVAVKMLKEASADMOADPQREALALAEFDNPIVLLGVCAGKPMCLLEFEMAY 651
DB 592 EPTMVAVKMLKEASADMOADPQREALALAEFDNPIVLLGVCAGKPMCLLEFEMAY 651
QY 661 GDLINEFRSMSPHTVCSLSHSDLSMRQVSSPGPPPLSCAEOLCIARQVAGMAYLSERK 720
DB 661 GDLINEFRSMSPHTVCSLSHSDLSMRQVSSPGPPPLSCAEOLCIARQVAGMAYLSERK 720
QY 652 GDLINEFRSMSPHTVCSLSHSDLSMRQVSSPGPPPLSCAEOLCIARQVAGMAYLSERK 711
DB 652 GDLINEFRSMSPHTVCSLSHSDLSMRQVSSPGPPPLSCAEOLCIARQVAGMAYLSERK 711
QY 721 FVHRDLATRNCLVGENNVVYKIADEGSLRNITYSADYKANENDAIPTMMPPESTFYRYT 780
DB 721 FVHRDLATRNCLVGENNVVYKIADEGSLRNITYSADYKANENDAIPTMMPPESTFYRYT 780
QY 712 FVHRDLATRNCLVGENNVVYKIADEGSLRNITYSADYKANENDAIPTMMPPESTFYRYT 771
DB 712 FVHRDLATRNCLVGENNVVYKIADEGSLRNITYSADYKANENDAIPTMMPPESTFYRYT 771
QY 781 TESDVAVYGVLMELFISYGLQPYGYMAHEEVIYVRDGNILSCPENCPVELYNMLRLCWS 840
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QY 772 TESDVAVYGVLMELFISYGLQPYGYMAHEEVIYVRDGNILSCPENCPVELYNMLRLCWS 831
DB 772 TESDVAVYGVLMELFISYGLQPYGYMAHEEVIYVRDGNILSCPENCPVELYNMLRLCWS 831
QY 841 KLPADRPSTSIHRIILERMCEERAGTVSV 869
DB 841 KLPADRPSTSIHRIILERMCEERAGTVSV 869
QY 832 KLPADRPSTSIHRIILERMCEERAGTVSV 860
DB 832 KLPADRPSTSIHRIILERMCEERAGTVSV 860

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RESULT 9  
CT-US95-08493-13  
Sequence 13, Application PC/TUS9508493

GENERAL INFORMATION:

APPLICANT: Wood, Clive  
APPLICANT: Caruso, Anthony  
TITLE OF INVENTION: Novel mlk Receptor Tyrosine Kinases  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESS: LEGAL AFFAIRS  
STREET: 87 Cambridge Park Drive  
CITY: Cambridge  
STATE: MA  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08493  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15234A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 946 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-08493-13

Query Match 63.4%; Score 2897; DB 5; Length 946;  
Best Local Similarity 59.9%; Pred. No. 3.6e-218;  
Matches 571; Conservative 113; Mismatches 159; Indels 100; Gaps 11;

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QY 5 VNPDLVHLLLVAFSGTEK--LKPAPVITTPLETVDAVLEEVATFCAVESYPOPEISWT 62
DB 6 VNPDLVHLLLVAFSGTEK--LKPAPVITTPLETVDAVLEEVATFCAVESYPOPEISWT 62
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DB 63 RNLILKLPDTRYSIRENGOLITLTVSEDDGGYCYCTANNNGAGANESGALQVKKPK 122
QY 65 RNNIPRPDTRYSIRENGOLITLTVSEDDGGYCYCTANNNGAGANESGALQVKKPK 124
DB 65 RNNIPRPDTRYSIRENGOLITLTVSEDDGGYCYCTANNNGAGANESGALQVKKPK 124
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DB 123 ITRPPIVAKIIEGLKAVLPCTYGNPKRPSVWIKGDSPLR-ENSRLAVLESGSLRIHNVQ 181
QY 125 ITRPPIVAKIIEGLKAVLPCTYGNPKRPSVWIKGDSPLR-ENSRLAVLESGSLRIHNVQ 184
DB 125 ITRPPIVAKIIEGLKAVLPCTYGNPKRPSVWIKGDSPLR-ENSRLAVLESGSLRIHNVQ 184
QY 182 KEDAGQRCYAKNSIGTAVSKVYKLEFEVFARLILRAPESHNVTPGSEVTLHCTATGIVP 241
DB 182 KEDAGQRCYAKNSIGTAVSKVYKLEFEVFARLILRAPESHNVTPGSEVTLHCTATGIVP 241
QY 185 LKQAGYTRCLARNSLGEFERSALAEVQASARIVKAPTSONVSYGSEVTLQCKATGPRIP 244
DB 185 LKQAGYTRCLARNSLGEFERSALAEVQASARIVKAPTSONVSYGSEVTLQCKATGPRIP 244
QY 242 TTIWINGNAVSSGSIQESYKDRVIDSRQLQITFKGGLYCIATNKHGEKFTAKAATIT 301
DB 242 TTIWINGNAVSSGSIQESYKDRVIDSRQLQITFKGGLYCIATNKHGEKFTAKAATIT 301
QY 245 TIKMLENGRAVPKGSIONRIKGEVMSRLVYVTRPSLFTCLTNKHNBSSTAKATATL 304
DB 245 TIKMLENGRAVPKGSIONRIKGEVMSRLVYVTRPSLFTCLTNKHNBSSTAKATATL 304
QY 302 SIEMSKPKQDNKGYCAQYRGEVCNAYLAKDALVFLNTSYADPEAEQELLVHTANNEKLV 361
DB 302 SIEMSKPKQDNKGYCAQYRGEVCNAYLAKDALVFLNTSYADPEAEQELLVHTANNEKLV 361
QY 305 DIKEM-RLKRGDGLQSTYRGEVCGGLNGOGLVFENSSPADAEQTEMARSTWELDG 363
DB 305 DIKEM-RLKRGDGLQSTYRGEVCGGLNGOGLVFENSSPADAEQTEMARSTWELDG 363
QY 362 VSPVCRAAEALACNHIPOECSP-GVAPPTPIPIREXCLAVKELEFCAKEMLVMEKTHRG 420
DB 362 VSPVCRAAEALACNHIPOECSP-GVAPPTPIPIREXCLAVKELEFCAKEMLVMEKTHRG 420
QY 364 VSLCKRPAESLILCHFTFDONCPILGIPPKVLCRCHCLAVKELEYKERTIMEDNSRIG 423
DB 364 VSLCKRPAESLILCHFTFDONCPILGIPPKVLCRCHCLAVKELEYKERTIMEDNSRIG 423
QY 421 LYRESEHMLSVKCSKIPSMHMDPTACARLPHLDYNNENKLTFFPMNISKSVIPNIPS 460
DB 421 LYRESEHMLSVKCSKIPSMHMDPTACARLPHLDYNNENKLTFFPMNISKSVIPNIPS 460
QY 424 VYASAG--LSLPCCQLPSIHNDPEACTVSEFLMKKKGLVTRWCYNNNGRFYGVNVA 480
DB 424 VYASAG--LSLPCCQLPSIHNDPEACTVSEFLMKKKGLVTRWCYNNNGRFYGVNVA 480
QY 461 -----KTPPMPTSS----- 469
DB 461 -----KTPPMPTSS----- 469
QY 481 SGISQORMSEQAPHFHRLRPELPELANSDNFCRNPGSESRPWCYTDNDRIRMERCNPV 540
DB 481 SGISQORMSEQAPHFHRLRPELPELANSDNFCRNPGSESRPWCYTDNDRIRMERCNPV 540
QY 470 -----KPSVDIPMLPSSSSSFVSPTYSMTVITISMSFAIFVLLITLTYCC 518
DB 470 -----KPSVDIPMLPSSSSSFVSPTYSMTVITISMSFAIFVLLITLTYCC 518
QY 541 OCINVSISSEMKPKTETANTPSTSA-----TYSMTVITISMSFAIFVLLITLTYCC 593
DB 541 OCINVSISSEMKPKTETANTPSTSA-----TYSMTVITISMSFAIFVLLITLTYCC 593
QY 519 RRRKQMKKK--RESAAVLTTLPLSELILDRHPNPMYORPRLNPKLLNPKLLNPKLLNPKLLN 576
DB 519 RRRKQMKKK--RESAAVLTTLPLSELILDRHPNPMYORPRLNPKLLNPKLLNPKLLNPKLLN 576
QY 594 HHQGLQTRKSYRTTETPTLATPLSELILDRHPNPMYORPRLNPKLLNPKLLNPKLLNPKLLN 653
DB 594 HHQGLQTRKSYRTTETPTLATPLSELILDRHPNPMYORPRLNPKLLNPKLLNPKLLNPKLLN 653
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DB 577 YVRDIGEAGFGRVFOARAGLLPYEPFTVAVKMLKEASADMOADPQREALALAEFDNPIV 636
QY 654 YVRDIGEAGFGRVFOARAGLLPYEPFTVAVKMLKEASADMOADPQREALALAEFDNPIV 713
DB 654 YVRDIGEAGFGRVFOARAGLLPYEPFTVAVKMLKEASADMOADPQREALALAEFDNPIV 713
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DB 774 LSCADQNLIAKQISGMYTYSERKRVHNDLARNCLVGENNVYKIADEGSLRNITYSADY 833
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DB 757 KANENDAIPIRMMPPESTFYRYTTSQVMAVGVLMELFISYGLQPYGYMAHEEVIYVR 816
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DB 834 KANENDAIPIRMMPPESTFYRYTTSQVMAVGVLMELFISYGLQPYGYMAHEEVIYVR 893
QY 817 DGNILSCPENCPVELYNMLRLCWSKLPADRPSTSIHRIILERMCEERAGTVSV 869
DB 817 DGNILSCPENCPVELYNMLRLCWSKLPADRPSTSIHRIILERMCEERAGTVSV 869

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Db 894 DGNILSCBENCPELYNMLRLCWSMPSDRPTFASIHRLERHQRMAALPV 946

## RESULT 10

PCT-US95-08493-2

Sequence 2, Application PC/TUS9508493

GENERAL INFORMATION:

APPLICANT: Wood, Clive

APPLICANT: Caruso, Anthony

TITLE OF INVENTION: Novel mlk Receptor Tyrosine Kinases

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESS: LEGAL AFFAIRS

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: MA

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/08493

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: G15234A

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 530 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-08493-2

Query Match 56.9%; Score 2597.5; DB 5; Length 530;

Best Local Similarity 90.4%; Pred. No. 4.3e-195;

Matches 487; Conservative 20; Mismatches 23; Indels 9; Gaps 2;

Db 331 KDAIVLNTSYADPEAQLVHTANNELKAVSPVCRPAEALLCHITQECSPGVVPTP 390

Db 1 KDAIVFNTSYRDEDAOELLHTANNELKAVSPICRPAEALLCHITQECSPGVVPTP 60

QY 391 IPICREYCLAVKELFCAKELVMEKTHRGILYSEMHLLSVPKCSKLPSEHMDPTACARL 450

QY 61 MPICREYCLAVKELFCAKELVMEKTHRGILYSEMHLLSVPKCSKLPSEHMDPTACARL 120

QY 451 PHLDYKNEKLTPEPTMTSKPSVDIPNLDSSTSSSTVSPTTYMTYIISINSFAIFVLL 510

Db 121 PYL-----AFPSITSSRPADIDNLP-ASTSSPAVSPTYSMTYIISIVSSFAIFALL 171

QY 511 TITLIVCCRRKCKKMKKRESAAVTLTTPSELIDBLHPNPMYQRMPLINLKLSLEY 570

Db 172 TITLIVCCRRKCKKMKKRESAAVTLTTPSELIDBLHPNPMYQRMPLINLKLSLEY 231

QY 571 PRNIEYVDIGEGAFGEVQARAPGLIPYEPPTMAVAVKMLKEBASADMOADFOREALM 630

Db 232 PRNIEYVDIGEGAFGEVQARAPGLIPYEPPTMAVAVKMLKEBASADMOADFOREALM 291

QY 631 AEPDNPITVLLGVCAVGRKPCMLLEFYMAGDINEFIRSMSPHTVCSLSHSDLSMRAOVS 690

Db 292 AEPDNPITVLLGVCAVGRKPCMLLEFYMAGDINEFIRSMSPHTVCSLSHSDLSMRAOVS 351

QY 691 SPGPPLSCAEOLCIAROVAAGMAYLSERKFVHRDLATRNCLVGENNVVRIADFGLSRNT 750

Db 691 SPGPPLSCAEOLCIAROVAAGMAYLSERKFVHRDLATRNCLVGENNVVRIADFGLSRNT 750

Db 352 SPGPPLSCAEOLCIAROVAAGMAYLSERKFVHRDLATRNCLVGENNVVRIADFGLSRNT 411

QY 751 YSAIYYANENDALPIRMMPESIFYNRYTSPDYAVGVIMEIFYSGLOPYGMAHEE 810

Db 412 YSADYVADGDNDALPIRMMPESIFYNRYTSPDYAVGVIMEIFYSGLOPYGMAHEE 471

QY 811 VIVYVROGNIILSCBENCPELYNMLRLCWSKLPADRPSTSIHRLERHQRMAALPV 869

Db 472 VIVYVROGNIILSCBENCPELYNMLRLCWSKLPADRPSTSIHRLERHQRMAALPV 530

RESULT 11

PCT-US95-08493-15

Sequence 15, Application PC/TUS9508493

GENERAL INFORMATION:

APPLICANT: Wood, Clive

APPLICANT: Caruso, Anthony

TITLE OF INVENTION: Novel mlk Receptor Tyrosine Kinases

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESS: LEGAL AFFAIRS

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: MA

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/08493

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: G15234A

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 478 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-08493-15

Query Match 50.6%; Score 2312; DB 5; Length 478;

Best Local Similarity 91.4%; Pred. No. 8e-173;

Matches 437; Conservative 19; Mismatches 22; Indels 0; Gaps 0;

QY 1 MRELVINIPVHILTLVAFSGTEKLPKAPVITPTEVTDAVLVEEATFMCAVSEYPOPEIS 60

Db 1 MRELVINIPVHILTLVAFSGTEKLPKAPVITPTEVTDAVLVEEATFMCAVSEYPOPEIS 60

QY 61 WTRNKLILKLFDRYSIRENGQLTLTIVSDSDGTYCCTANNVGAVESGALQVKK 120

Db 61 WTRNKLILKLFDRYSIRENGQLTLTIVSDSDGTYCCTANNVGAVESGALQVKK 120

QY 121 PKTRPPINVKITIEGKAVLPCTTMGNPKPSVSMIKGDSPLRENSRIAVLESGLRIHNV 180

Db 121 PKTRPPINVKITIEGKAVLPCTTMGNPKPSVSMIKGDSPLRENSRIAVLESGLRIHNV 180

QY 181 OKEDAGQYRCVANSJGTAVSKYKLEFEYFAILAPESHNTFSGVTLHGTATGIVP 240

Db 181 OKEDAGQYRCVANSJGTAVSKYKLEFEYFAILAPESHNTFSGVTLHGTATGIVP 240

QY 241 PTITWENGNAVSSGSIQESVNDVDSRLQLFTFRGALTCTATNKGKSTARAAT 300

Db 241 PTITWENGNAVSSGSIQESVNDVDSRLQLFTFRGALTCTATNKGKSTARAAT 300

QY 241 PTITWENGNAVSSGSIQESVNDVDSRLQLFTFRGALTCTATNKGKSTARAAT 300

Db 241 PTITWENGNAVSSGSIQESVNDVDSRLQLFTFRGALTCTATNKGKSTARAAT 300

QY 301 ISIAEWSKPOKNGYCAQYRGEVCNNAVLAKDALVFLNTSYADEPEAOELLVHTANWELK 360  
Db 301 VSIANEWSKQSDSGYCAQYRGEVCNNAVLAKDALVFLNTSYADEPEAOELLVHTANWELK 360  
QY 361 VSVSVCPRAAEALICNHIIFQECSPGVVPTPIPIREYCLAVKELFCAKEMLVMEKTHRG 420  
Db 361 AVSFLCPRAAEALICNHIIFQECSPGVVPTPIPIREYCLAVKELFCAKEMLVMEKTHRG 420  
QY 421 LYREEMHLLSVKCSKLPMSHMDPTACARLPHLDYKNENLKTFFPMSSKPSVDIPNL 478  
Db 421 LYRGMHLLVPECSKLPMSHMDPTACTRLPYLDYKNENLKTFFPMSSKPSVDIPNL 478

## RESULT 12

US-08-701-191A-30  
Sequence 30, Application US/08701191A  
Patent No. 5943428

## GENERAL INFORMATION:

APPLICANT: Moosa Mohammadi, Joseph Schlessinger,  
and Stevan R. Hubbard  
TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FASTSEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/701,191A  
FILING DATE: August 21, 1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

## FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 227/088  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

## INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:  
LENGTH: 304 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-701-191A-30

Query Match 34.5%; Score 1577; DB 2; Length 304;  
Best Local Similarity 97.0%; Pred. No. 1,3e-115;  
Matches 295; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 562 NPKLLSLEYPRNNIEYVDIGEGAFGRVFOARAPGLPEPTMVAVKMLKEEASADMA 621  
Db 1 NPKLLSLEYPRNNIEYVDIGEGAFGRVFOARAPGLPEPTMVAVKMLKEEASADMA 60  
QY 622 DFOREAAALAEFDNPNITVLLGVCAVGRKPMCLLFEXMAYGDLNEFLRMSPTVCSLSHS 681  
Db 61 DFOREAAALAEFDNPNITVLLGVCAVGRKPMCLLFEXMAYGDLNEFLRMSPTVCSLSHS 120

QY 682 DLSRAVSSBPPLSCAEOLCIAROVAAGMAYLSERKTVHRDLATRNCLVGENMYVKI 741  
Db 121 DLSRAVSSBPPLSCAEOLCIAROVAAGMAYLSERKTVHRDLATRNCLVGENMYVKI 180  
QY 742 ADFGLSRNITSADYKKNENDAPIRMPPESTIFYNRYTESDVAAGVYLMETFSYGLQ 801  
Db 181 ADFGLSRNITSADYKKNENDAPIRMPPESTIFYNRYTESDVAAGVYLMETFSYGLQ 240  
QY 802 PYGMAHEEVIYYVRDGNILSCENCPVELYNMRLCWSKLPADRPSTSIHRLERMC 861  
Db 241 PYGMAHEEVIYYVRDGNILSCENCPVELYNMRLCWSKLPADRPSTSIHRLERMC 300  
QY 862 RAEK 865  
Db 301 RAEK 304

## RESULT 13

US-08-469-537A-105  
Sequence 105, Application US/08469537A  
Patent No. 5843749

## GENERAL INFORMATION:

APPLICANT: Maisongier, et al.  
TITLE OF INVENTION: EHK AND ROR TYROSINE  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
STREET: 777 Old Saw Mill River Road  
CITY: Tarrytown  
STATE: NY  
COUNTRY: U.S.A.  
ZIP: 10591

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,537A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/406,247  
FILING DATE: 17-MAR-1995

## APPLICATION NUMBER: USSN 08/144,992

FILING DATE: 28-OCT-1993  
APPLICATION NUMBER: USSN 07/736,559  
FILING DATE: 26-JUL-1991

## ATTORNEY/AGENT INFORMATION:

NAME: Kempler, Ph.D., Gall M  
REGISTRATION NUMBER: 32,143  
REFERENCE/DOCKET NUMBER: REG 07/0C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 914-345-7400  
TELEFAX: 914-345-7721  
TELEX:

## INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:  
LENGTH: 937 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: Internal

NAME/KEY: Human ROR1  
LOCATION: 1...937  
OTHER INFORMATION:

US-08-469-537A-105

Query Match 19.7%; Score 899; DB 2; Length 937;

```

MEDIAN TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,537A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 07/736,559
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Ph.D., Gail M
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 070C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
TELEX:
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Human ROR2
LOCATION: 1...943
OTHER INFORMATION:
US-08-469-537A-107
Query Match 19.2%; Score 876; DB 2; Length 943;
Best Local Similarity 28.6%; Pred. No. 4,7e-60;
Matches 236; Conservative 119; Mismatches 249; Indels 222; Gaps 26;
QY 126 PPIVKIIIEGLAKVILECTTGMGPKPSVSWIGKDSPLRENSRAVL---ESGS-LRIHWQ 181
Db 67 PVNNITIIQOGTALIHCKVGNPNPNVWMLKNDALVQVEPRRIIRKTEYGRLLIQQD 126
QY 182 KEDAGQYRCVAKNSLGTATYSKVKVLEFVFVARILRAPESHNVTFGSEFVTLHCTATGIPVP 241
Db 127 TTIDGIYQCAVFNKMT-----ITANGV--- 149
QY 242 TITWINGNAVSSGSIOESVKDRIYDSRLQLFITRPGLYTCLATNKKHGEKFTAKAAFI 301
Db 150 -----LFV-----RLGPTH 158
QY 302 SLAEWSKPKQDNKGCAQYRGFEVNAVLAKDALVELNTSYADPEEAQ---ELLVHTANNE 358
Db 159 SPNNHFQDDYHEDGDCQPRIGIACARFTGN-----RTIYDSLOMGSGIENRIITAFTM 212
QY 359 LKV---VSPVCRPAEALLCNHIFQEC-SPGVVPTPIPCREYCLAVKELFCAKELVME 414
Db 213 IGTSHLSDDQSOFAIPSCFHFVPLCDARSRAKPRREICRDECEVLESDLCROEYTA- 271
QY 415 EKTNGGLYRSE---WHLSVPRCSLPSMHMDPTA---CARLP-----HLDN--- 456
Db 272 -----RSLNPLILMRLOLPRCEALP-MPESPDAKNCRIITPAERLGRYHOCTYNGSGM 322
QY 457 -----KENLKTFP-----PMTSSKPSVDIPNL----- 478
Db 323 DYRGIASTTKSGHQOCPALMDHNRHHLSSTDFPELGGGHAYCRNPGOMEGSPMCFQNK 382
QY 479 -----PSSSSSFSVSPYISMTVIISMSRAI-FVLLTITLLYC-CRRRQMK 527
Db 383 NVRMELCDVPCSPSPDSS-----KKGIIYILVPSIAIPLVIACLFELVCMCR-----NK 431

```

RESULT 15  
 US-08-339-578-2  
 Sequence 2, Application US/08339578  
 Patent No. 5622862  
 GENERAL INFORMATION:  
 APPLICANT: Squinto, et al.  
 TITLE OF INVENTION: ASSAY SYSTEMS FOR NEUROTROPHIN ACTIVITY  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
 STREET: 777 Old Saw Mill River Road  
 CITY: Tarrytown  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10591-6707  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/339,578  
 FILING DATE: 14-NOV-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/690,199  
 FILING DATE: 23-APR-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kempner, Gall M.  
 REGISTRATION NUMBER: 32,143  
 REFERENCE/DOCKET NUMBER: 6526-061A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (914) 345-7400  
 TELEFAX: (914) 345-7721  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 821 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-339-578-2

```

Query Match      18.9%  Score 862;  DB 1;  Length 821;
Best Local Similarity 28.5%  Pred. NO. 4.8e-59;
Matches 259;  Conservative 121;  Mismatches 254;  Indels 276;  Gaps 34.

34 LETVDALVEEATGMCAGVESTPOPEISNTKILIKLFDTRYISRE-----NQO 82
|  || : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Db 96 LIIIVDSGLKFAV-YKAFKLSNLRHINFTNRNKI-----TSLRRHRHLDLSDLITLGN 148

QY 83 -----LIIILSVESDD--GIYCTANNG-----VGAVESGALGVKKPKITRP 126

Db 149 PFTCSODIMMLKTLOETKSSPDPTDOLCLINSSKNMPLANLOIPRNGL-----PSARLA 202

QY 127 PIVNKLIELKAVLCTTGMGNKRPSTWYKGD-----SPLRENSFIAVLESGLRIHNVQKE 183

Db 203 APNLVVEREKSVTLSOSVGGDPLPYLVWGNILVSKNMETHSH-----TQSLRITINISD 258

QY 184 DAG-OYRCVAKNSLGTAVSKV-VKLEFEVFARILRAPESHN---VYFGSPVLHCAATGI 238

Db 259 DSGKQISCAEVLVGEDDSVNLGVHFAPTIFLESPTDHMCIF-----TVRGH 310

QY 239 PVPITTLIENGNAVSSGSIQESVKRVIDSR-----LOLETKR-----GLVTCIATNRH 288

Db 311 KPRLQWYNG-ALINESKYICTKLIHNTETYNCSOL--DNPTMNGNDYTLMAKNRY 367

QY 289 GEKESTAKAAATISIAEWSKPKQDKGCAOYRGECVAVLKDALLVFLNTSYADEENO 348

Db 368 G-----KDRQISAHNG-----380

QY 349 ELIVHTANMLKVSPVCRPAEALLCNHIFQESRGVVPPIPICTREXCLAVKELFCAK 408

Db 381 -----RPGVD-----YETNP-----HYPEVLTE-----398

QY 409 EMLVMEKTHRGLEXSEMHILTVPCSKLPSMHNDPTCARPLHLDYKKNKIKTPRMTS 468

Db 399 DWTI-----PDIIDGTI-----NKS-----414

QY 469 SKSPVDIPNLPESSSSSEFSPTYSMTVIISIMSFALVLLTTLTYCCRRRKOMKK 528

Db 415 EIPSTDVAD-QSREHLSV--YAVVYIASVG--FCLVMLLLKLARHSGFGKG 465

QY 529 RESAVLITLPLSELDDLRLHPNMYO-----RMLPLNPKL 565

Db 466 PAVY-----ISNDDASAPLIHISNCSNTPSSSEGGPDVAITIGMTIPIYENPOY 515

QY 566 LSL-----EYRNNEIYVRDIEGAGFVFCARAPGLIPLREPFMAVAVKMLE 613

Db 516 FGITNSQLKPDTEVOHAIKRHNIVYKRELGEAGFKVFLAEQYNLCRPEQDKLIVAVKTLK- 574

QY 614 EASADQADQOREFALMAEFNDPIVYLLVCAVANGKRMCLLFETVMAVGDLEBTRLSMPH 673

Db 575 DADNMRKDPHRAELITLNQHETIYAFVGCVEGDDLIVFEFKYMGKDLKFFIRAPGPD 634

QY 674 TVCSLSHSDLSMRQVSSPGPPP--LSCADQLCIARQVAAGAMAYLSERKFVHRDLATRNC 731

Db 635 AV-----LMAEGNPTELTQSGMLIAQIAGMWYLAQHGYHRLATRNC 681

QY 732 LVGENNVYKIDRGLSRNITSADYKXANENDALPIRMKRPESIFYNRITTESDVAAYGV 791

Db 682 LVGENLTVKIDGKMSRDVISTDYRARGGHTMLPIRMKRPESIMYRKFTTESDWSIGVV 741

QY 792 LMEIFSGLQPYGMAHEEVIYVDRGNLISCPENFVELYINLMRLCWSKLPADRPSETS 851

Db 742 LMEIFEYKQPMYOLSNNEVIECTITQGVLYQRRTRICQEVYELMLGCMQREPHTRKNKS 801

QY 852 IHRILERMCE 861

Db 802 IHTLQNLNLA 811

Search completed: June 18, 2003, 10:30:03  
Job time : 22 secs

